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- ° This is a continuation-in-part application of U.S. Serial No. 08/385,998, filed February 9, 1995.

Title of Invention

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF TUMOR GENE INT6.

5

Field of Invention

- 10 The present invention relates to the area of cancer diagnostics and therapeutics. More specifically, the invention relates to the *Int6* gene and to the use of
reagents derived from the nucleic acid and deduced amino acid sequences of the *Int6* gene in gene therapy, vaccines,
15 diagnostic methods and immunotherapy.

Background of Invention

- 20 The mouse mammary tumor virus (MMTV) is a retrovirus which has been shown to act as an insertional mutagen that causes the deregulation of expression of cellular genes adjacent to the site of MMTV integration in mammary tumors (Varmus, H.E. (1982). Cancer Surv., 1:309-320). Mice infected with MMTV frequently develop preneoplastic hyperplastic alveolar nodules (HAN) (Daniel, C., et al.
25 Proc. Natl. Acad. Sci. USA., 61:53-60; DeOme, K.B., (1959) J. Natl. Cancer Inst., 78:751-757; Medina, D., (1973) Methods Cancer Res., 7:3-53; Smith, G., et al. (1984) Cancer Res., 44:3426-3437) and the passage of these nodules in cleared mammary fat pads of syngeneic mice by
30 serial outgrowth often results in the development of mammary tumors within these mice in a stochastic manner. In addition, it is not uncommon to find metastatic lesions in the lungs of mice bearing outgrowths with mammary tumors. For these reasons, there is considerable interest
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in identifying MMTV-induced mutational events that may contribute to different stages of tumor development.

Using the MMTV genome as a molecular tag, five loci (*Wnt-1/Int-1*, *Fgf-3/Int-2*, *Int-3*, *Wnt-3*, and *Fgf-4/Hst/k-FGF*) have been identified which represent common

5 integration sites (designated *Int* loci) for MMTV in mouse mammary tumors (Dickson, C., et al. (1984) Cell., 37:529-536; Gallahan, D., et al. (1987) J. Virol., 61:218-220; Nusse, R., et al. (1982) Cell., 31:99-109; Peters, G., et al. (1989) Proc. Natl. Acad. Sci. USA., 86:5678-5682).
10 Transgenic mouse studies utilizing transgenes in which the MMTV LTR was linked to either the *WNT-1*, *Fgf-3*, or *Int-3* genes have demonstrated that activation of expression of these genes contributes to mammary tumorigenesis (Jhappan, C., et al. (1992) Genes & Develop., 6:345-355; Muller, W.J., et al. (1990) Embo J., 9:907-913; Tsukamoto, A.S., et al. (1988) Cell., 55:619-625).

The present invention describes the isolation of a new *Int* gene designated *Int6* and the use of the gene, its gene product, and reagents derived from the gene and its
20 gene product, in diagnostic methods, vaccines, immunotherapy and gene therapy.

Summary of Invention

25 The present invention relates to the isolation of the *Int6* gene. The invention also relates to the murine and human cDNAs which comprise the coding sequence of the *Int6* gene. The invention further relates to nucleic acid sequences derived from the *Int6* gene and the *Int6* cDNAs and the use of these nucleic acid sequences as probes to
30 isolate homologues of the *Int6* gene in other mammals or as probes to detect mutations of the *Int6* gene.

It is also an object of the present invention to provide synthetic nucleic acid sequences capable of directing production of recombinant *Int6* protein and
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° peptide fragments derived therefrom, as well as equivalent natural nucleic acid sequences. Such natural nucleic acid sequences may be isolated from a cDNA or genomic library from which the gene capable of directing the synthesis of the *Int6* protein may be identified and isolated. For the purposes of this application, nucleic acid sequence refer to RNA, DNA, cDNA or any synthetic variant thereof.

The present invention further relates to *Int6* protein and peptides derived therefrom.

The invention also relates to antibodies directed against *Int6* protein or peptides derived therefrom.

The invention also provides methods for detecting mutations of *Int6* gene where detection of such mutations is useful in determining the presence of a neoplastic tissue in a subject or a genetic predisposition to cancer in a subject.

A first method for detecting mutations of the *Int6* gene comprises analyzing DNA of a subject for mutations of the *Int6* gene.

A second method for detecting mutations of the *Int6* gene comprises analyzing RNA of a subject for alterations in the *Int6* mRNA expression.

Yet another method for detecting mutations of the *Int6* gene comprises analyzing protein of a subject for alterations in *Int6* protein expression.

The present invention also provides pharmaceutical compositions for use as vaccines for immunizing a subject against cancer and for use in immunotherapy methods. One such composition comprises nucleic acid sequence capable of directing host organism synthesis of *Int6* protein or peptide fragments thereof while a second pharmaceutical composition comprises *Int6* protein or peptides derived therefrom.

The above pharmaceutical compositions may also be used in immunotherapy methods for treating a subject having cancer. For use in immunotherapy, the present

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invention further provides a third pharmaceutical composition comprising antibodies directed against *Int6* protein or peptides derived therefrom where such antibodies are coupled to toxin molecules, radioisotopes or drugs.

5 The present invention therefore relates to application of immunotherapy to subjects having cancer comprising administering one or more of the above pharmaceutical compositions to said subject in a therapeutically effective amount.

10 The invention further relates to a method for treating a subject having cancer comprising:

(a) immunizing the subject with an amount of an expression vector encoding *Int6* protein or with *Int6* protein itself, said amount effective to elicit a specific
15 T cell response;

(b) isolating said T cells from said immunized subject; and

(c) administering said T cells to said immunized subject or to an unimmunized subject in a
20 therapeutically effective amount.

The invention also provides a diagnostic kit for determining the nucleotide sequence of *Int6* alleles by the polymerase chain reaction, said kit comprising purified and isolated nucleic acid sequences useful as PCR primers.
25 These PCR primers are also useful in analyzing DNA or RNA of a subject for mutations of the *Int6* gene.

The present invention further provides a method for supplying the wild-type *Int6* gene to a cell having altered expression of the *Int6* protein by virtue of a mutation in
30 the *Int6* gene, the method comprising: introducing a wild-type *Int6* gene into a cell having altered expression of the *Int6* protein such that said wild-type gene is expressed in the cell.

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Description of Figures

Figures 1A and 1B show the results of Southern blot analyses in which 10 micrograms of cellular DNA was digested by EcoRI, separated by agarose gel electrophoresis, and hybridized with MMTV LTR probe. In Figure 1A, the DNAs analyzed were isolated from a CZZ-1 pre-neoplastic hyperplastic outgrowth line designated CZZ-1 HOG (lane 1) and from CZZ-1 derived mammary tumors 22 (lane 2), 1262 (lane 3), 1263 (lane 4), 20 (lane 5), 19 (lane 6), 23 (lane 7), 21 (lane 8), 24 (lane 9), 8 (lane 10), 9 (lane 11), 12 (lane 12), 13 (lane 13) and 14 (lane 14) as indicated at the top of Figure 1A. In Figure 1B, the DNAs analyzed were isolated from CZZ-1 derived tumor 4973 (lane 1) and from 11 independent lung metastasis (lanes 2-12) from a mouse bearing tumor 4973 as indicated at the top of Figure 1B.

Figures 2A-2C show the results of Southern blot analyses of 10 micrograms of cellular DNA digested with EcoRI, separated by agarose gel electrophoresis and hybridized as follows. Lanes 1 and 2 of the blots in Figures 2A and 2B were hybridized with probe D which corresponds to host flanking sequences. Lane 2 of the blots in Figures 2A and 2B was subsequently hybridized with MMTV gag sequences (a 2.0 kb-Pst-XhoI fragment from MMTV GR-40; Gallahan and Callahan J. Virol, 61, 66-74: (1987)) and the results are shown in lane 3 in Figures 2A and 2B. Lanes 1 and 2 in Figure 2C were hybridized with probe C. Lane 2 was subsequently hybridized with MMTV env sequences (1.7 kb PstI fragment from MMTV (C3H); Gallahan and Callahan J. Virol, 61: 66-74; (1987)) and the result is shown in lane 3 in Figure 2C. The DNAs analyzed were isolated from CZZ-1 HOG derived tumor 22 (Figure 2A, lanes 2 and 3), independent mammary tumor 1139 (Figure 2B, lanes 2 and 3) independent mammary tumor 3134 (Figure 2C, lanes 2 and 3), and normal liver. (Lane 1 in Figures 2A-2C). The

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presence of the arrow in Figures 2A-2C indicates the site of the MMTV induced rearranged restriction fragment. The locations of probes C and D in the *Int6* gene are shown in Figure 3.

Figure 3 is a schematic diagram of the murine *Int6* locus in which the location of the four overlapping lambda clones which span the *Int6* locus (designated 1 to 4) are shown relative to a partial restriction map of sites for EcoRI (E), XbaI (X), PstI (P), BglII (BGL), HindIII (H), and BamHI (B) in the *Int6* locus. The location of the *Int6* exons and of restriction fragments used as probes A-D are indicated below the restriction map by solid and hatched boxes respectively. The scale of the restriction map is given in increments of 1.0 kb at the bottom of the Figure while the location and transcriptional orientation of integrated MMTV proviral genomes within the *Int6* gene of tumors 1139 and 3144, or within the *Int6* gene of the CZZ-1 HOG, is indicated by arrowheads above the restriction map.

Figure 4 shows the results of Northern blot analysis of total RNA isolated from *Int6* negative tumor (tumor 178) and the *Int6* positive tumors (22 and 1139). The RNAs were denatured in the presence of formaldehyde, separated on a 1% agarose gel containing formaldehyde, and hybridized with probe A.

Figure 5 shows the complete nucleotide sequence of the murine 1.4 kb *Int6* cDNA where intron breaks are indicated by small arrows (▲) above the start of the next exon and the deduced amino acid sequence of the gene product is given below the nucleotide sequence. Potential phosphorylation sites for cyclic AMP/cyclic GMP-dependent protein kinase (o), protein kinase C (Δ), tyrosine kinases (-), casein kinase II (∇), and glycosylation sites (□) are indicated in the deduced amino acid sequence.

Abbreviations for amino acid residues: A, Ala; C, Cys; D, Asp; E, Glu; F, Phe; G, Gly; H, His; I, Ile; K, Lys; M.

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- ° Met; N, Asn; P, Pro; Q, Gln; R, Arg; S, Ser; T, Thr; V, Val; W, Trp; Y, Tyr.

Figure 6 shows the results of a "Zoo" blot in which cellular DNA (10 µg each) isolated from *C. Elegans*, *Drosophila*, *Xenopus*, chicken, mouse and human was hybridized with *Int6* cDNA under high stringency conditions.

Figure 7 shows the results of Northern blot analyses of total RNA (10 µg each) isolated from normal adult tissues (top panel) and from developing embryos (lower panel). The RNAs were denatured in the presence of formaldehyde, run on 1% agarose gels containing formaldehyde and then transferred to a nylon membrane and hybridized sequentially with a β -actin-probe (the 2.3 kb mRNAs) and then a murine *Int6* cDNA probe (the 1.4 kb mRNAs).

Figure 8 shows a schematic illustrating the location and nucleotide sequence of a cryptic transcription stop signal (underlined) in the reverse sequence of the MMTV LTR where the sequence shown corresponds to bases 464 through 497 from the three prime end of the LTR. The hatched box corresponds to an *Int6* exon and the open box corresponds to the LTR of an integrated MMTV proviral genome integrated within *Int6*. The U5, R and U3 regions of the MMTV LTR are indicated as well as the transcriptional orientations of the MMTV genome and the *Int6* gene.

Figures 9A and 9B show the nucleotide sequences of the junctions between MMTV and *Int6* sequences in chimeric *Int6*-MMTV LTR RNA species detected in tumors 1139 (Figure 9A) and 22 (Figure 9B). In Figure 9A, the nucleotide sequence shown begins at the 5' end of exon with the nucleotide sequence shown in lower case letters corresponding to intron 5 sequences. Amino acid sequences in RNA species 2 which are identical to those in RNA species 1 are indicated by dots and nucleotide sequences

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° which have been spliced out in RNA species 2 are indicated by dashes. Nucleotide and amino acid sequences which are underlined are from the integrated MMTV genome.

In Figure 9B, the nucleotide sequence shown for the chimeric RNA species detected in tumor 22 begins at the 5' end of exon 9 and run through a portion of intron 9 to the cryptic poly A addition signal in the MMTV genome. Intron nucleotide sequence is given in lower case letters, MMTV sequences are underlined, and dashes indicate nucleotide sequences of the intron which have been spliced out. Dots correspond to amino acid residues encoded by RNA species 2 and 3 which are identical to those encoded by RNA species 1. The abbreviations for amino acids shown in Figures 9A and 9B are the same as those given in the legend for Figure 5.

15 Figure 10 shows the genomic map of the human *Int6* gene. As in the mouse genome, the human *Int6* gene is composed of 13 exons (filled bars) where the nucleotide boundaries for each exon are presented in the Figure. The location of a CA-repeat sequence in the seventh intron is also shown.

20 Figure 11 shows the nucleotide sequence of primers (underlined) complementary to the nucleic acid sequences (not underlined) flanking the CA-repeat in intron 7 of the human *Int6* gene. The distance of the primers from the CA-repeat are presented as 40 and 138 base pairs respectively and the number of CA-repeats (18) shown is that found in the wild-type *Int6* gene. The upper nucleic acid sequences are shown in the 5' to 3' orientation and the lower nucleic acid sequences are shown in the 3' to 5' orientation reading left to right.

30 Figure 12 shows the results of Southern blots in which human DNA (lane 4), Chinese hamster-human somatic cell hybrid DNA containing only human chromosome 6 (lane 1) or human chromosome 8 (lane 2) and mouse-human somatic cell hybrid DNA which contains human chromosomes 3,7,8,15

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- ° and 17 (lane 3) were digested with Hind III and hybridized with human *Int6* cDNA.

Figure 13 shows the results of PCR amplification of DNA from primary human breast tumor (T) and matching normal tissue (L, where L indicates lymphocyte) using labelled primers flanking the CA repeat sequence in intron 7 of the *Int6* gene. The numbers above each blot represent patients from which tumor and matching normal tissue samples were obtained. The arrow next to each blot indicates the complete loss, or a significantly reduced signal, of one allele relative to the matching normal DNA.

Figure 14 shows the nucleotide sequences bounding 12 of the 13 human *Int6* exons. Nucleotide sequences of primers (underlined) complementary to nucleic acid sequences (not underlined) bounding each exon are shown to the left and right of each exon. The upper nucleic acid sequences shown to the left and right of each exon are in the 5' to 3' orientation while lower sequences shown to the left and right of each exon are in the 3' to 5' orientation. When the sequences bounding each exon do not begin at the intron-exon junction, the distance of the sequence from the junction is given in base pairs to the left or right of each exon.

Figure 15 shows the results of a Northern blot of total RNA (20µg each) isolated from primary breast tumor (T) and matching normal (N) tissue. The RNA samples were denatured in the presence of formaldehyde, run on 1% agarose gels containing formaldehyde, then transferred to a nylon membrane and hybridized sequentially with a β -actin-probe and a human *Int6* cDNA probe.

Figure 16 shows the results of a Northern blot of total RNA (20µg each) isolated from human nonsmall cell lung carcinomas (54T and 55T) and matching normal tissue (55N). Matching normal tissue for 54T was also surveyed for *Int6* mRNA expression but the Northern blot for 54N is

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- ° not shown. Northern blot analysis was carried out as described in Figure 15.

DESCRIPTION OF INVENTION

5 The present invention discloses that mutational events associated with MMTV integration into the host cell genome in tumorigenesis occur in a previously unknown gene designated *Int6*. This gene is located on mouse chromosome 15. More specifically, the present invention relates to *Int6* gene and its corresponding cDNA. The region of mouse
10 chromosome 15 containing the *Int6* is represented in the four overlapping lambda clones (designated 1-4 in Figure 3) and comprises the entire *Int6* gene. The *Int6* gene represents the wild-type *Int6* gene.

15 The present invention is also directed to the full-length cDNA corresponding to the murine *Int6* gene. This cDNA sequence is set forth below as SEQ ID NO:1.

| | | | | | |
|----|------------|------------|------------|------------|------|
| | AACAAGCGCT | CCTTTCCCCC | GGCAAGATGG | CGGAGTACGA | 40 |
| | CCTGACTACT | GCATCGCGCA | TTTTCTGGAT | CGGCACCTGG | 80 |
| | TCTTTCCGCT | TCTTGAGTTT | CTCTCTGTGA | AAGAGATTTA | 120 |
| 20 | TAATGAAAAA | GAATTATTAC | AAGGAAAATT | AGATCTTCTT | 160 |
| | AGTGATACCA | ATATGGTGA | CTTTGCTATG | GATGTTTACA | 200 |
| | AAAACCTTTA | TTCTGATGAT | ATCCCTCATG | CTTTGAGAGA | 240 |
| | AAAAAGAACC | ACAGTTGTTG | CGCAGCTGAA | ACAGCTCCAG | 280 |
| | GCAGAAACAG | AACCAATTGT | GAAGATGTTT | GAAGATCCAG | 320 |
| | AAACTACAAG | GCAGATGCAG | TCAACCAGGG | ATGGCAGGAT | 360 |
| | GTTATTTGAC | TACCTGGCAG | ACAAACATGG | GTTTAGGCAA | 400 |
| 25 | GAGTACTTAG | ATACACTCTA | CAGATACGCA | AAATTCCAGT | 440 |
| | ATGAGTGTGG | AAATTACTCT | GGAGCTGCAG | AGTATCTTTA | 480 |
| | CTTCTTTAGA | GTTTTGGTCC | CAGCAACAGA | TAGAAATGCT | 520 |
| | TTAAGTTCGC | TCTGGGGAAA | ACTGGCCTCT | GAAATCTTAA | 560 |
| | TGCAGAATTG | GGATGCAGCC | ATGGAAGACC | TTACTCGATT | 600 |
| | AAAAGAAACC | ATAGACAATA | ATTCTGTGAG | TTCTCCACTC | 640 |
| | CAGTCTCTTC | AGCAGCGAAC | ATGGCTCATT | CATTGGTCTC | 680 |
| | TATTTGTTTT | TTTCAACCAT | CCAAAGGGCC | GTGATAACAT | 720 |
| 30 | TATTGATCTC | TTCCTTTACC | AACCACAGTA | TCTTAATGCA | 760 |
| | ATTCAGACAA | TGTGTCCACA | TATTCTACGC | TATTTGACTA | 800 |
| | CTGCCGTCAT | AACCAACAAA | GATGTGCGGA | AACGCCGGCA | 840 |
| | GGTGCTGAAA | GATCTGGTGA | AAGTGATTCA | ACAGGAGTCT | 880 |
| | TACACATATA | AAGACCCAAT | TACAGAAATT | GTTGAATGCC | 920 |
| | TATATGTTAA | CTTTGATTTT | GACGGGGCTC | AGAAAAAGCT | 960 |
| | GAGAGAATGT | GAATCAGTGC | TCGTGAATGA | CTTCTTCCTG | 1000 |
| 35 | GTAGCGTGTC | TGGAGGACTT | CATTGAGAAT | GCCCGTCTCT | 1040 |

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° TCATATTTGA GACGTTTTGT CGTATCCACC AGTGTATCAG 1080
 CATTAAATATG TTAGCAGATA AACTGAATAT GACTCCAGAA 1120
 GAAGCTGAAA GATGGATTGT GAATTTGATT AGAAATGCGA 1160
 GGTTGGATGC CAAGATTGAT TCTAAACTAG GTCATGTGGT 1200
 AATGGGCAAC AATGCAGTCT CGCCCTACCA GCAAGTGATT 1240
 GAAAAGACCA AAAGCCTTTC TTTTAGAAGC CAAATGTTGG 1280
 CCATGAATAT TGAAAAGAAA CTTAATCAGA ACAGTAGATC 1320
 5 AGAGGCTCCC AACTGGGCAA CCCAAGACTC TGGCTTCTAT 1360
 TAAAGGATTA TAAAGAAAAG AAGAAAAAGG AATAAGTGAA 1400
 AGACACAGTA GCCATTGTGT ATAAAGGATG ACATACATTT 1440
 TTAGAAGCAA TTAACATGTT TGCTACAAAT TTTGGAGAAT 1480
 TTGAATAAAA TTGGCTATGA TTA 1504

10 The abbreviation used for the nucleotides are those
 standardly used in the art.

The deduced amino acid sequence of the murine *Int6*
 cDNA is shown as SEQ ID NO:2 below and starts at
 nucleotide 173 of SEQ ID NO:1 and extends 1188
 nucleotides.

15 Met Val Asp Phe Ala Met Asp Val Tyr Lys Asn Leu
 1 5 10
 Tyr Ser Asp Asp Ile Pro His Ala Leu Arg Glu Lys
 15 20
 Arg Thr Thr Val Val Ala Gln Leu Lys Gln Leu Gln
 25 30 35
 Ala Glu Thr Glu Pro Ile Val Lys Met Phe Glu Asp
 40 45
 20 Pro Glu Thr Thr Arg Gln Met Gln Ser Thr Arg Asp
 50 55 60
 Gly Arg Met Leu Phe Asp Tyr Leu Ala Asp Lys His
 65 70
 Gly Phe Arg Gln Glu Tyr Leu Asp Thr Leu Tyr Arg
 75 80
 Tyr Ala Lys Phe Gln Tyr Glu Cys Gly Asn Tyr Ser
 85 90 95
 25 Gly Ala Ala Glu Tyr Leu Tyr Phe Phe Arg Val Leu
 100 105
 Val Pro Ala Thr Asp Arg Asn Ala Leu Ser Ser Leu
 110 115 120
 Trp Gly Lys Leu Ala Ser Glu Ile Leu Met Gln Asn
 125 130
 30 Trp Asp Ala Ala Met Glu Asp Leu Thr Arg Leu Lys
 135 140
 Glu Thr Ile Asp Asn Asn Ser Val Ser Ser Pro Leu
 145 150 155
 Gln Ser Leu Gln Gln Arg Thr Trp Leu Ile His Trp
 160 165
 Ser Leu Phe Val Phe Phe Asn His Pro Lys Gly Arg
 170 175 180
 35 Asp Asn Ile Ile Asp Leu Phe Leu Tyr Gln Pro Gln

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0 Tyr Leu Asn Ala 185 190
 195 200
 Leu Arg Tyr Leu Thr Thr Ala Val Ile Thr Asn Lys
 205 210 215
 Asp Val Arg Lys Arg Arg Gln Val Leu Lys Asp Leu
 220 225
 5 Val Lys Val Ile Gln Gln Glu Ser Tyr Thr Tyr Lys
 230 235 240
 Asp Pro Ile Thr Glu Phe Val Glu Cys Leu Tyr Val
 245 250
 Asn Phe Asp Phe Asp Gly Ala Gln Lys Lys Leu Arg
 255 260
 Glu Cys Glu Ser Val Leu Val Asn Asp Phe Phe Leu
 265 270 275
 10 Val Ala Cys Leu Glu Asp Phe Ile Glu Asn Ala Arg
 280 285
 Leu Phe Ile Phe Glu Thr Phe Cys Arg Ile His Gln
 290 295 300
 Cys Ile Ser Ile Asn Met Leu Ala Asp Lys Leu Asn
 305 310
 Met Thr Pro Glu Glu Ala Glu Arg Trp Ile Val Asn
 315 320
 15 Leu Ile Arg Asn Ala Arg Leu Asp Ala Lys Ile Asp
 325 330 335
 Ser Lys Leu Gly His Val Val Met Gly Asn Asn Ala
 340 345
 Val Ser Pro Tyr Gln Gln Val Ile Glu Lys Thr Lys
 350 355 360
 Ser Leu Ser Phe Arg Ser Gln Met Leu Ala Met Asn
 365 370
 20 Ile Glu Lys Lys Leu Asn Gln Asn Ser Arg Ser Glu
 375 380
 Ala Pro Asn Trp Ala Thr Gln Asp Ser Gly Phe Tyr
 385 390 395

25 The present invention also discloses the nucleotide
 sequence of the human homologue of the *Int6* cDNA where the
 human *Int6* cDNA sequence is 89% homologous to the mouse
 sequence. Two overlapping recombinant clones (HINT6A and
 HINT6B) represent the 5' and 3' halves respectively of the
 human *Int6* cDNA sequence. These two clones were deposited
 30 with the American Type Culture collection (ATCC), 12301
 Parklawn Drive, Parkville, MD 20852 on January 24, 1995
 and have ATCC accession numbers 97029 and 97030. The human
Int6 cDNA sequence is shown below as SEQ ID NO:3.

35 ACTCCCTTTT CTTTGGCAAG ATGGCGGAGT ACGACTTGAC
 TACTCGCATC GCGCACTTTT TGGATCGGCA TCTAGTCTTT

40
80

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| | | | | | |
|----|-------------|-------------|------------|-------------|------|
| 0 | CCGCTTCTTG | AATTTCTCTC | TGTAAAGGAG | ATATATAATG | 120 |
| | AAAAGGAATT | ATTACAAGGT | AAATTGGACC | TTCTTAGTGA | 160 |
| | TACCAACATG | GTAGACTTTG | CTATGGATGT | ATACAAAAAC | 200 |
| | CTTTATTCTG | ATGATATTCC | TCATGCTTTG | AGAGAGAAAA | 240 |
| | GAACCACAGT | GGTTGCACAA | CTGAAACAGC | TTCAGGCAGA | 280 |
| | AACAGAACCA | ATTGTGAAGA | TGTTTGAAGA | TCCAGAAACT | 320 |
| | ACAAGGCAAA | TGCAGTCAAC | CAGGGATGGT | AGGATGCTCT | 360 |
| 5 | TTGACTACCT | GGCGGACAAG | CATGGTTTTA | GGCAGGAATA | 400 |
| | TTTAGATACA | CTCTACAGAT | ATGCAAAATT | CCAGTACGAA | 440 |
| | TGTGGGAATT | ACTCAGGAGC | AGCAGAATAT | CTTTATTTTT | 480 |
| | TTAGAGTGCT | GGTTCAGCA | ACAGATAGAA | ATGCTTTAAG | 520 |
| | TTCACTCTGG | GGAAAGCTGG | CCTCTGAAAT | CTTAATGCAG | 560 |
| | AATTGGGATG | CAGCCATGGA | AGACCTTACA | CGGTTAAAAG | 600 |
| | AGACCATAGA | TAATAATTCT | GTGAGTTCTC | CACTTCAGTC | 640 |
| | TCTTCAGCAG | AGAACATGGC | TCATTCACTG | GTCTCTGTTT | 680 |
| 10 | GTTTTCTTCA | ATCACCCCAA | AGGTCGCGAT | AATATTATTG | 720 |
| | ACCTCTTCCT | TTATCAGCCA | CAATATCTTA | ATGCAATTCA | 760 |
| | GACAATGTGT | CCACACATTC | TTCGCTATTT | GACTACAGCA | 800 |
| | GTCATAACAA | ACAAGGATGT | TCGAAAACGT | CGGCAGGTTT | 840 |
| | TAAAAGATCT | AGTTAAAGTT | ATTCAACAGG | AGTCTTACAC | 880 |
| | ATATAAAGAC | CCAATTACAG | AATTTGTTGA | ATGTTTATAT | 920 |
| | GTTAACTTTG | ACTTTGATGG | GGCTCAGAAA | AAGCTGAGGG | 960 |
| 15 | AATGTGAATC | AGTGCTTG TG | AATGACTTCT | TCTTGGTG GC | 1000 |
| | TTGTCTTGAG | GATTTCAATTG | AAAATGCCCG | TCTCTTCATA | 1040 |
| | TTTGAGACTT | TCTGTGCGCAT | CCACCAGTGT | ATCAGCATT A | 1080 |
| | ACATGTTG GC | AGATAAATTG | AACATGACTC | CAGAAGAAGC | 1120 |
| | TGAAAGGTGG | ATTGTAAATT | TGATTAGAAA | TGCAAGACTG | 1160 |
| | GATGCCAAGA | TTGATTCTAA | ATTAGGTCAT | GTGGTTATGG | 1200 |
| | GTAACAATGC | AGTCTCACCC | TATCAGCAAG | TGATTGAAAA | 1240 |
| | GACCAAAAGC | CTTTCCTTTA | GAAGCCAGAT | GTTGGCCATG | 1280 |
| 20 | AATATTGAGA | AGAACTTAA | TCAGAATAGC | AGGTCAGAGG | 1320 |
| | CTCCTAACTG | GGCAACTCAA | GATTCTGGCT | TCTACTGAAG | 1360 |
| | AACCATAAAG | AAAAGATGAA | AAAAAAACT | ATCAAAGAAA | 1400 |
| | GATGAAATAA | TAAAACTATT | ATATAAAGGG | TGACTTACAT | 1440 |
| | TTTGGAACAA | ACATATTACG | TATAAATTTT | GAAGAATTGG | 1480 |
| | AATAAAATTG | ATTCATTTTA | | | 1500 |

25 The deduced amino acid sequence of the human *Int6* cDNA is shown below as SEQ ID NO:4 and starts at nucleotide 168 of SEQ ID NO:3 and extends 1188 nucleotides.

| | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Met | Val | Asp | Phe | Ala | Met | Asp | Val | Tyr | Lys | Asn | Leu |
| | 1 | | | | 5 | | | | | 10 | | |
| 30 | Tyr | Ser | Asp | Asp | Ile | Pro | His | Ala | Leu | Arg | Glu | Lys |
| | | | 15 | | | | | 20 | | | | |
| | Arg | Thr | Thr | Val | Val | Ala | Gln | Leu | Lys | Gln | Leu | Gln |
| | 25 | | | | | 30 | | | | 35 | | |
| | Ala | Glu | Thr | Glu | Pro | Ile | Val | Lys | Met | Phe | Glu | Asp |
| | | | | 40 | | | | | 45 | | | |
| 35 | Pro | Glu | Thr | Thr | Arg | Gln | Met | Gln | Ser | Thr | Arg | Asp |
| | | 50 | | | | | 55 | | | | | 60 |

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° Gly Arg Met Leu Phe Asp Tyr Leu Ala Asp Lys His
 65 70
 Gly Phe Arg Gln Glu Tyr Leu Asp Thr Leu Tyr Arg
 75 80
 Tyr Ala Lys Phe Gln Tyr Glu Cys Gly Asn Tyr Ser
 85 90 95
 Gly Ala Ala Glu Tyr Leu Tyr Phe Phe Arg Val Leu
 100 105
 5 Val Pro Ala Thr Asp Arg Asn Ala Leu Ser Ser Leu
 110 115 120
 Trp Gly Lys Leu Ala Ser Glu Ile Leu Met Gln Asn
 125 130
 Trp Asp Ala Ala Met Glu Asp Leu Thr Arg Leu Lys
 135 140
 10 Glu Thr Ile Asp Asn Asn Ser Val Ser Ser Pro Leu
 145 150 155
 Gln Ser Leu Gln Gln Arg Thr Trp Leu Ile His Trp
 160 165
 Ser Leu Phe Val Phe Phe Asn His Pro Lys Gly Arg
 170 175 180
 Asp Asn Ile Ile Asp Leu Phe Leu Tyr Gln Pro Gln
 185 190
 15 Tyr Leu Asn Ala Ile Gln Thr Met Cys Pro His Ile
 195 200
 Leu Arg Tyr Leu Thr Thr Ala Val Ile Thr Asn Lys
 205 210 215
 Asp Val Arg Lys Arg Arg Gln Val Leu Lys Asp Leu
 220 225
 Val Lys Val Ile Gln Gln Glu Ser Tyr Thr Tyr Lys
 230 235 240
 20 Asp Pro Ile Thr Glu Phe Val Glu Cys Leu Tyr Val
 245 250
 Asn Phe Asp Phe Asp Gly Ala Gln Lys Lys Leu Arg
 255 260
 Glu Cys Glu Ser Val Leu Val Asn Asp Phe Phe Leu
 265 270 275
 Val Ala Cys Leu Glu Asp Phe Ile Glu Asn Ala Arg
 280 285
 25 Leu Phe Ile Phe Glu Thr Phe Cys Arg Ile His Gln
 290 295 300
 Cys Ile Ser Ile Asn Met Leu Ala Asp Lys Leu Asn
 305 310
 Met Thr Pro Glu Glu Ala Glu Arg Trp Ile Val Asn
 315 320
 30 Leu Ile Arg Asn Ala Arg Leu Asp Ala Lys Ile Asp
 325 330 335
 Ser Lys Leu Gly His Val Val Met Gly Asn Asn Ala
 340 345
 Val Ser Pro Tyr Gln Gln Val Ile Glu Lys Thr Lys
 350 355 360
 Ser Leu Ser Phe Arg Ser Gln Met Leu Ala Met Asn
 365 370
 35 Ile Glu Lys Lys Leu Asn Gln Asn Ser Arg Ser Glu

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| | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---------|
| | | 375 | | | | 380 | | | | | |
| | Ala | Pro | Asn | Trp | Ala | Thr | Gln | Asp | Ser | Gly | Phe Tyr |
| 385 | | | | | | 390 | | | | | 395 |

The amino acid sequence of human and mouse *Int6* proteins are identical.

5 Variations are contemplated in the cDNA sequences shown in SEQ ID NOS:1 and 3 which will result in a DNA sequence that is capable of directing production of analogs of the proteins shown in SEQ ID NOS:2 and 4 respectively. It should be noted that the DNA sequences
10 set forth above represents a preferred embodiment of the present invention. Due to the degeneracy of the genetic code, it is to be understood that numerous choices of nucleotides may be made that will lead to a DNA sequence capable of directing production of the instant *Int6*
15 proteins or their analogs. As such, DNA sequences which are functionally equivalent to the sequence set forth above or which are functionally equivalent to sequences that would direct production of analogs of the *Int6* proteins produced pursuant to the amino acid sequences set
20 forth above, are intended to be encompassed within the present invention.

The term analog includes any protein or polypeptide having an amino acid residue sequence substantially identical to a sequence specifically shown herein in which
25 one or more amino acid residues have been conservatively substituted with a functionally similar residue. Examples of conservative substitutions include, for example, the substitution of one non-polar (i.e. hydrophobic) residue such as isoleucine, valine, leucine or methionine for
30 another; the substitution of one polar (i.e. hydrophilic) residue for another, such as a substitution between arginine and lysine, between glutamine and asparagine, or between glycine and serine; the substitution of one basic residue such as lysine, arginine or histidine for another;

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- ° or the substitution of one acidic residue, such as aspartic acid or glutamic acid for another.

The phrase conservative substitution may also include the use of a chemically derivatized residue in place of a non-derivatized residue.

- 5 Chemical derivative refers to an *Int6* protein or polypeptide having one or more residues chemically derivatized by reaction of a functional side group. Examples of such derivatized molecules include, but are not limited to, those molecules in which free amino groups
- 10 have been derivatized to form, for example, amine hydrochlorides, p-toluene sulfonyl groups, carbobenzoxy groups, t-butyloxycarbonyl groups, chloroacetyl groups or formyl groups. Free carboxyl groups may be derivatized to form salts, methyl and ethyl esters, or other types of
- 15 esters or hydrazides. Free hydroxyl groups may be derivatized to form O-acyl or O-alkyl derivatives. The imidazole nitrogen of histidine may be derivatized to form N-im-benzylhistidine. Also included as chemical derivatives are those proteins or peptides which contain
- 20 one or more naturally-occurring amino acid derivatives of the twenty standard amino acids. For example, 4-hydroxyproline may be substituted for proline; 5-hydroxylsine may be substituted for histidine; homoserine may be substituted for serine; and ornithine may be
- 25 substituted for lysine.

- The nucleic acid sequences provided by the present invention are useful as probes for a number of purposes. For example, they can be used as probes in Southern hybridization to genomic DNA and in the RNase protection
- 30 method for detecting point mutations. The probes can be used to detect PCR amplification products. They may also be used to detect mismatches with the *Int6* gene or mRNA using other techniques. Mismatches can be detected using either enzymes (e.g., S1 nuclease), chemicals (e.g.,
- 35 hydroxylamine or osmium tetroxide and piperidine), or

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changes in electrophoretic mobility of mismatched hybrids as compared to totally matched hybrids. These techniques are known in the art. The probes are complementary to *Int6* gene coding sequences, although probes to introns are also contemplated. An entire battery of nucleic acid probes is used to compose a kit for detecting alteration of wild-type *Int6* genes. The kit allows for hybridization to the entire *Int6* gene. The probes may overlap with each other or be contiguous.

If a riboprobe is used to detect mismatches with mRNA, it is complementary to the mRNA of the human wild-type *Int6* gene. The riboprobe thus is an anti-sense probe in that it does not code for the *Int6* protein because it is of the opposite polarity to the sense strand. The riboprobe generally will be labeled with a radioactive, colorimetric, or fluorometric materials, which can be accomplished by any means known in the art. If the riboprobe is used to detect mismatches with DNA it can be of either polarity, sense or anti-sense. Similarly, DNA probes also may be used to detect mismatches.

Nucleic acid probes may also be complementary to mutant alleles of *Int6* gene. These allele-specific probes are useful to detect similar mutations in other patients on the basis of hybridization rather than mismatches. As mentioned above, the *Int6* probes can also be used in Southern hybridizations to genomic DNA to detect gross chromosomal changes such as deletions and insertions. The probes can also be used to select cDNA clones of *Int6* genes from tumor and normal tissues. In addition, the probes can be used to detect *Int6* mRNA in tissues to determine if expression is altered as a result of mutation of wild-type *Int6* genes. Provided with the *Int6* gene and the *Int6* cDNA sequences shown in SEQ ID NOs:1 and 3, design of particular probes is well within the skill of the ordinary artisan.

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0 The present invention also relates to methods for detecting mutations of the *Int6* gene in a subject.

For purposes of the present invention, subject means a mammal and mutation means inversion, translocation, insertion, deletion or point mutation of the wild-type
5 *Int6* gene.

It is believed that many mutations found in tumor tissues will be those leading to altered expression of *Int6* protein. However, mutations leading to non-functional gene products can also lead to cancer. It is
10 further understood that point mutations can occur in regulatory regions (e.g. promoter) or can disrupt proper RNA processing thus leading to reduced *Int6* mRNA
— expression or loss of expression of the *Int6* protein respectively.

15 The fact that integration of MMTV into the *Int6* gene is observed in preneoplastic mouse mammary lesions suggests that mutations of *Int6* are involved in early events of cancer. The methods of detecting mutations of the *Int6* gene can therefore provide diagnostic and
20 prognostic information. For example, detection of mutation of the *Int6* gene in a tumor may effect the course of treatment chosen by a clinician. The methods of the present invention are applicable to any tumor in which mutations of *Int6* occur. Loss of expression of the *Int6*
25 gene has been observed in tumors of the lung and breast. Thus, these are tumors in which *Int6* has a role in tumorigenesis. In addition, since *Int6* is expressed in all tissues tested including brain, heart, kidney, liver, ovaries, spleen and testes, mutations affecting the
30 expression of the *Int6* gene may contribute to neoplasia in these tissues too. Finally, since lung and breast tumors are derived from epithelial tissue, the methods of the invention may be useful in the detection of epithelial cell derived cancers such as nonsmall cell lung
35 carcinomas.

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° It is further understood by one skilled in the art that the methods for detection disclosed in the present invention can be used prenatally to screen a fetus or presymptomatically to screen a subject at risk of having cancer based on his/her family history.

5 In one embodiment of the invention, the method for detecting mutations of the *Int6* gene comprises analyzing the DNA of a subject for mutations of the wild-type *Int6* gene. For analysis of DNA, a biological specimen is obtained from the subject. Examples of biological
10 specimens that can be obtained for use in the present method, include, but are not limited to, tissue biopsies and blood. Means for enriching a tissue preparation for tumor cells are known in the art. For example, the tissue may be isolated from paraffin or cryostat sections.
15 Cancer cells may also be separated from normal cells by flow cytometry. These as well as other techniques for separating tumor from normal cells are well known in the art. Alternatively, primary cell cultures can be established from tumor biopsies using methods known to
20 those of ordinary skill in the art.

The DNA isolated from the biological specimen can be analyzed for mutations of the *Int6* gene by a variety of methods including Southern blotting after digestion with the appropriate restriction enzymes (restriction fragment
25 length polymorphism, RFLP) (Botstein, D. Amer. J. Hum. Genet. (1980) 69:201-205, denaturing gradient electrophoresis technique (Myers, R.M., Nature (1985) 313:495-498), oligonucleotide hybridization (Conner, R. et al., EMBO J. (1984) 3:13321-1326), RNase digestion of a
30 duplex between a probe RNA and the target DNA (Winter, E. et al., Proc. Natl. Acad. Sci. U.S.A. (1985) 82:7575-7579), polymerase chain reaction (PCR) (Saiki, P.K. et al., Science (1988) 239:487-491; U.S. Patents 4,683,195 and 4,683,202), ligase chain reaction (LCR) (European
35 Patent Application Nos. 0,320,308 and 0,439,182), and PCR-

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- ° single stranded conformation analysis (PCR-SSCP) (Orita, M. et al., Genomics (1989) 5:874-879; Dean, M. et al. Cell (1990) 61:863-871).

In one preferred embodiment, Southern blot analysis can be used to examine tumor or blood DNA for gross rearrangement of the *Int6* gene. The DNA to be analyzed via Southern analysis is digested with one or more restriction enzymes. Following restriction digestion, resultant DNA fragments are separated by gel electrophoresis and the fragments are detected by hybridization with a labelled nucleic acid probe. (Southern, E.M. J. Mol. Biol. (1975) 98:503-517).

The nucleic acid sequence used as a probe in Southern analysis can be labeled in single-stranded or double-stranded form. Labelling of the nucleic acid sequence can be carried out by techniques known to one skilled in the art. Such labelling techniques can include radiolabels and enzymes (Sambrook, J. et al. (1989) in "Molecular Cloning, A Laboratory Manual", Cold Spring Harbor Press, Plainview, New York). In addition, there are known non-radioactive techniques for signal amplification including methods for attaching chemical moieties to pyrimidine and purine rings (Dale, R.N.K. et al. (1973) Proc. Natl. Acad. Sci., 70:2238-2242; Heck, R.F. 1968) S. Am. Chem. Soc., 90:5518-5523), methods which allow detection by chemiluminescence (Barton, S.K. et al. (1992) J. Am. Chem. Soc., 114:8736-8740) and methods utilizing biotinylated nucleic acid probes (Johnson, T. K. et al. (1983) Anal. Biochem., 133:126-131; Erickson, P.F. et al. (1982) J. of Immunology Methods, 51:241-249; Matthaei, F.S. et al. (1986) Anal. Biochem., 157:123-128) and methods which allow detection by fluorescence using commercially available products. The size of the probe can range from about 200 nucleotides to about several kilobases. A preferred probe size is about 500 to about 2000 nucleotides. The probe may be derived from introns or

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exons of the *Int6* gene. Each of the nucleic acid sequences used as a probe in Southern analysis is substantially homologous to the corresponding portion of the murine or human *Int6* genes where these genes have the cDNA sequences shown in SEQ ID NOs:1 or 3 respectively.

5 In a preferred embodiment, the probes are derived from a human *Int6* gene having the *Int6* cDNA sequence shown in SEQ ID NO:3. By "substantially homologous" is meant a level of homology between the nucleic acid sequence used as a probe and the corresponding sequence of the human or
10 murine *Int6* genes. Preferably, the level of homology is in excess of 70%, most preferably in excess of 80%, with a particularly preferred nucleic acid sequence being in
—excess of—90% homologous with—the sequence of the mouse or human *Int6* genes.

15 Once the separated DNA fragments are hybridized to the labelled nucleic acid probes, the restriction digest pattern can be visualized by autoradiography and examined for the presence or absence of a restriction fragment length polymorphism (RFLP) associated with mutation of the
20 *Int6* gene.

In another preferred embodiment, genomic DNA may be analyzed for mutations in the *Int6* gene via PCR-SSCP. In this method, each of the pair of primers selected for use in PCR are designed to hybridize with sequences in the
25 *Int6* gene to permit amplification and subsequent detection of mutations in the denatured amplification product via non-denaturing polyacrylamide gel electrophoresis. In a preferred embodiment, primer pairs are derived from the human *Int6* gene. In a more preferred embodiment, primer
30 pairs are derived from intronic sequences which border the 5' and 3' ends of a given exon of the human *Int6* gene. Examples of primer pairs permitting specific amplification of the exons of the human *Int6* gene include, but are not limited to,

35 SEQ ID NO:5

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° ACCAATAAAGTTTTAGTGAGCACAG
SEQ ID NO:6
GCGCCCAAAGACCCCTCAC
SEQ ID NO:7
TTAATCAGTTTCTTTGGGGA
5 SEQ ID NO:8
AGTTTCTAATGACAAACTTAC
SEQ ID NO:9
TCTTCTGCATTTTAAATTAG
SEQ ID NO:10
10 CAAAATTAAGACGAGTTTAC
SEQ ID NO:11
CTTATTTTGTTTCTGTGGCC
SEQ ID NO:12
CATGACAACCTTAAAATATTTTT
15 SEQ ID NO:13
AATTACAATGGGGTTTTAAA
SEQ ID NO:14
GAAGAACCAAGGGAATCCTA
SEQ ID NO:15
20 TTCAAGAGTATTCACAATAT
SEQ ID NO:16
TGTGAAAAAGACGAACTCAC
SEQ ID NO:17
AGTTTTCTTTATCTCACCTT
25 SEQ ID NO:18
CAATATATATTTTAGTTTAC
SEQ ID NO:19
CCGTTGACTTATTTTACAG
SEQ ID NO:20
30 AAATAAAAATTCACACTTAC
SEQ ID NO:21
TTGTTGTATTTGTACATATAG
SEQ ID NO:22
ATCAAATCACGGTGTTCTTAC
35 SEQ ID NO:23

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° AAAACTAAGTTTTTAGGCCC
SEQ ID NO:24
ATAGCTAACATAATACTCAC
SEQ ID NO:25
TTCCCTGTGTTTCCTTTTAG
5 SEQ ID NO:26
ATAGAAGATGTGTGGTCTTAC
SEQ ID NO:27
GATTTCTTTTTGCATATTTTAG
SEQ ID NO:28
10 CAAGAAAAGTACAGCAAGA

where SEQ ID NOs: 5 and 6 bound exon 1, SEQ ID NOs: 7 and 8 bound exon 2, SEQ ID NOs: 9 and 10 bound exon 3, SEQ ID NOs: 11 and 12 bound exon 4, SEQ ID NOs: 13 and 14 bound exon 5, SEQ ID NOs: 15 and 16 bound exon 6, SEQ ID NOs: 17 and 18 bound exon 8, SEQ ID NOs: 19 and 20 bound exon 9, SEQ ID NOs: 21 and 22 bound exon 10, SEQ ID NOs: 23 and 24 bound exon 11, SEQ ID NOs: 25 and 26 bound exon 12, and SEQ ID NOs: 27 and 28 bound exon 13. Optimization of the amplification reaction to obtain sufficiently specific hybridization to *Int6* gene sequences is well within the skill in the art and is preferably achieved by adjusting the annealing temperature.

The primers of this invention can be synthesized using any of the known methods of oligonucleotide synthesis (e.g., the phosphodiester method of Agarwal et al. 1972. *Agnew. Chem. Int. Ed. Engl.* 11:451, the phosphotriester method of Hsiung et al. 1979. *Nucleic Acids Res.* 6:1371, or the automated diethylphosphoramidite method of Beaucage et al. 1981. *Tetrahedron Letters* 22:1859-1862), or they can be isolated fragments of naturally occurring or cloned DNA. In addition, those skilled in the art would be aware that oligonucleotides can be synthesized by automated instruments sold by a variety of manufacturers or can be commercially custom ordered and prepared. In one embodiment, the primers can

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be derivatized to include a detectable label suitable for detecting and/or identifying the primer extension products (e.g., biotin, avidin, or radiolabeled dNTP's), or with a substance which aids in the isolation of the products of amplification (e.g. biotin or avidin).

5 In an alternative embodiment, primer pairs can be selected to hybridize to mutant forms of the *Int6* disease gene. The selected primer pairs will hybridize sufficiently specifically to the mutated gene sequences such that non-specific hybridization to wild-type *Int6*
10 gene sequences will not prevent identification of the amplification product of the mutant gene sequence. Primer pairs which hybridize to mutations in the *Int6* gene sequence can be used to amplify specific mutant gene sequences present in the DNA of a biological sample.

15 The amplification products of PCR can be detected either directly or indirectly. Direct detection of the amplification products is carried out via labelling of primer pairs. Labels suitable for labelling the primers of the present invention are known to one skilled in the art and include radioactive labels, biotin, avidin,
20 enzymes and fluorescent molecules. The desired labels can be incorporated into the primers prior to performing the amplification reaction. A preferred labelling procedure utilizes radiolabeled ATP and T4 polynucleotide kinase
25 (Sambrook, J. et al. (1989) in "Molecular Cloning, A Laboratory Manual", Cold Spring Harbor Press, Plainview, NY). Alternatively, the desired label can be incorporated into the primer extension products during the amplification reaction in the form of one or more labelled
30 dNTPs. In the present invention, the labelled amplified PCR products can be analyzed for mutations of the *Int6* gene via separating the PCR products by non-denaturing polyacrylamide gel electrophoresis, denaturing polyacrylamide gel electrophoresis (PCR-SSCP) or via
35 direct sequencing of the PCR-products.

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° In yet another embodiment, unlabelled amplification products can be analyzed for mutations in the *Int6* disease gene via hybridization with nucleic acid probes radioactively labelled or, labelled with biotin, in Southern blots or dot blots. Nucleic acid probes useful
5 in the embodiment are those described earlier for Southern analysis. In yet another embodiment, detection of point mutations may be accomplished by molecular cloning of the allele present in the tumor tissue using the cDNA sequences set forth in SEQ ID NOs:1 and 3 and sequencing
10 that allele using techniques well known in the art.

In a second embodiment, the method for detecting mutations of the *Int6* gene comprises analyzing the RNA of a subject for alterations in *Int6*-specific mRNA expression.

15 For the analysis of RNA by this method, RNA can be isolated from blood or a tumor biopsy sample obtained from said subject where said tumors include, but are not limited to, tumors of the breast and lung.

The RNA to be analyzed can be isolated from blood or
20 tumor biopsy samples as whole cell RNA or as poly(A)⁺ RNA. Whole cell RNA can be isolated by methods known to those skilled in the art. Such methods include extraction of RNA by differential precipitation (Birnbom, H.C. (1988) Nucleic Acids Res., 16:1487-1497), extraction of RNA by
25 organic solvents (Chomczynski, P. et al. (1987) Anal. Biochem., 162:156-159) and extraction of RNA with strong denaturants (Chirgwin, J.M. et al. (1979) Biochemistry, 18:5294-5299). Poly(A)⁺ RNA can be selected from whole cell RNA by affinity chromatography on oligo-d(T) columns
30 (Aviv, H. et al. (1972) Proc. Natl. Acad. Sci., 69:1408-1412). A preferred method of isolating RNA is extraction of whole cell RNA by acid-phenol (Chomczynski et al. 1987).

The methods for analyzing the RNA for alterations in
35 the pattern or level of *Int6*-specific mRNA expression

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° include Northern blotting (Alwine, J.C. et al. (1977) Proc. Natl. Acad. Sci., 74:5350-5354), dot and slot hybridization (Kafatos, F.C. et al. (1979) Nucleic Acids Res., 7:1541-1522), filter hybridization (Hollander, M.C. et al. (1990) Biotechniques; 9:174-179), RNase protection
5 (Sambrook, J. et al. (1989) in "Molecular Cloning, A Laboratory Manual", Cold Spring Harbor Press, Plainview, NY), reverse-transcription polymerase chain reaction (RT-PCR) (Watson, J.D. et al. (1992) in "Recombinant DNA" Second Edition, W.H. Freeman and Company, New York) and
10 RT-PCR-SSCP. One preferred method is Northern blotting.

The nucleic acid sequence used as a probe for detecting Int6-specific mRNA expression is substantially homologous to SEQ. ID. NOS. 1 or 3. By "substantially homologous" is meant a level of homology between the
15 nucleic acid sequence and the cDNA sequence of SEQ ID NOS:1 or 3. Preferably, the level of homology is in excess of 70% more preferably in excess on 80%, with a particularly preferred nucleic acid sequence being in excess of 90% homologous with the cDNA sequence shown in
20 SEQ ID Nos. 1 or 3.

In a second preferred embodiment, the RNA is analyzed for mutations in the Int6 gene by RT-PCR-SSCP. Single stranded cDNA is prepared from either tumor total RNA or polyA⁺ enriched RNA using reverse transcriptase. In this
25 method, each of the pairs of primers selected for use in PCR of the resultant single-stranded cDNA are designed to hybridize with sequences in the Int6 cDNA which are an appropriate distance apart (at least about 100-300 nucleotides) in the gene to permit amplification and
30 subsequent detection of mutations in the denatured amplification product via non-denaturing polyacrylamide gel electrophoresis. Primer pairs which can specifically hybridize to overlapping Int6 gene sequences can be derived from the Int6 gene sequence. Primer pairs can be
35 derived from the cDNA sequences set forth in SEQ ID NOS 1

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and 3. In a preferred embodiment, the primers are derived from the human *Int6* cDNA sequence shown in SEQ ID NO:3. Each primer of a pair is a single-stranded oligonucleotide of about 15 to about 20 bases in length which is complementary to a sequence at the 3' end of one of the strands of a double-stranded target sequence. Each pair comprises two such primers, one of which is complementary 3' end and the other of which is complementary to the other 3' end of the target sequence. The target sequence is generally about 100 to about 300 base pairs long. Optimization of the amplification reaction to obtain sufficiently specific hybridization to the *Int6* cDNA is well within the skill in the art and is preferably achieved by adjusting the annealing temperature. Alternatively, the denatured RT-PCR products can be analyzed for mutations of the *Int6* gene via direct sequencing of the RT-PCR products.

Yet another preferred method of analysis is the RNase protection method, which is described in detail in Winter et al., Proc. Natl. Acad. Sci. USA, 82: p. 7575, (1985) and Meyers et al., Science, 230: p 1242, (1985). In the practice of the present invention the method involves the use of a labeled riboprobe which is complementary to the human wild-type gene coding sequence. The riboprobe and either mRNA or DNA isolated from the tumor tissue are annealed (hybridized) together and subsequently digested with the enzyme RNase A which is able to detect mismatches in a duplex RNA structure. If a mismatch is detected by RNase A, it cleaves at the site of the mismatch. The riboprobe need not be the full length of the RNA or gene but can be a segment of either. If the riboprobe comprises only a segment of the *Int6* RNA or *Int6* gene it will be desirable to use a number of these probes to screen the whole mRNA sequence for mismatches.

The present invention also encompasses recombinant proteins derived from the cDNAs shown in SEQ ID Nos. 1 and

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3. Recombinant Int6 proteins can be produced by recombinant DNA methodology known to one skilled in the art. Since the amino acid sequence of mouse (SEQ ID NO:2) and human (SEQ ID NO:4) Int6 proteins are identical, a suitable nucleic acid sequence capable of encoding a protein comprising all or part of the amino acid sequence shown in SEQ ID NO:4 is the sequence shown in SEQ ID NO:3 or in SEQ ID NO:1. In a preferred embodiment, such a suitable nucleic acid sequence can be cloned into a vector capable of being transferred into, and replicated in, a host organism.

The vectors contemplated for use in the present invention include any vectors into which a nucleic acid sequence as described above can be inserted, along with any preferred or required operational elements, and which vector can then be subsequently transferred into a host organism and replicated in such organism. Preferred vectors are those whose restriction sites have been well documented and which contain the operational elements preferred or required for transcription of the nucleic acid sequence.

The "operational elements" as discussed herein include at least one promoter, at least one operator, at least one leader sequence, at least one terminator codon, and any other DNA sequences necessary or preferred for appropriate transcription and subsequent translation of the vector nucleic acid. In particular, it is contemplated that such vectors will contain at least one origin of replication recognized by the host organism along with at least one selectable marker and at least one promoter sequence capable of initiating transcription of the nucleic acid sequence.

In construction of the cloning vector of the present invention, it should additionally be noted that multiple copies of the nucleic acid sequence and its attendant operational elements may be inserted into each vector. In

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° such an embodiment, the host organism would produce greater amounts per vector of the desired *Int6* protein. The number of multiple copies of the DNA sequence which may be inserted into the vector is limited only by the ability of the resultant vector due to its size, to be transferred into and replicated and transcribed in an appropriate host microorganism.

In another embodiment, restriction digest fragments containing a coding sequence for *Int6* protein can be inserted into a suitable expression vector that functions in prokaryotic or eukaryotic cells. By suitable is meant that the vector is capable of carrying and expressing a complete nucleic acid sequence coding for *Int6* protein. ~~Examples of expression vectors that function in~~ prokaryotic cells such as bacteria include, but are not limited to, T7 promoter based vectors and vectors for producing *trpE* and *lacZ* fusions. Preferred expression vectors are those that function in a eukaryotic cell. Examples of such vectors include but are not limited to, vaccinia virus vectors, adenovirus, herpesviruses, baculovirus or mammalian type C retroviral vectors.

The selected recombinant expression vector may then be transfected into a suitable eukaryotic cell system for purposes of expressing the recombinant protein. Such eukaryotic cell systems include, but are not limited to cell lines such as human MCF10A or mouse HC11 mammary epithelial cells. One preferred eukaryotic cell system for use with baculovirus vectors is SF21 ovarian cells from spodoptera frugiperda.

The expressed recombinant protein may be detected by methods known in the art which include Coomassie blue staining and Western blotting using sera containing anti-*Int6* antibody.

In a further embodiment, the expressed recombinant protein can be obtained as a crude lysate or it can be purified by standard protein purification procedures known

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in the art which may include differential precipitation, molecular sieve chromatography, ion-exchange chromatography, isoelectric focusing, gel electrophoresis, affinity, and immunoaffinity chromatography and the like. In the case of immunoaffinity chromatography, the recombinant protein may be purified by passage through a column containing a resin which has bound thereto antibodies specific for the Int6 protein.

In yet another embodiment, the present invention relates to peptides derived from the Int6 amino acid sequences shown in SEQ ID Nos. 2 and 4 where those skilled in the art would be aware that the peptides of the present invention, or analogs thereof, can be synthesized by automated instruments sold by a variety of manufacturers, can be commercially custom ordered and prepared, or can be expressed from suitable expression vectors as described above. The term analog has been previously described in the specification and for purposes of describing peptides of the present invention, analogs can further include branched or non-linear peptides. Preferred peptides are those that range from about 20 to about 24 amino acids length and are immunogenic. As described in Example 8 herein, mutation of the Int6 gene can result in truncation of the expressed Int6 protein. Based on previous studies indicating that point-mutated ras proteins are processed in an appropriate manner to be targets for specific T cell-mediated cytotoxicity (Tsang; K.Y. et al. (1994) Vaccine Research, 3:183-193; Takahashi, H.S.; et al. (1989) Science, 246:118-121, Jung, S.; et al. (1991) J. Exp. Med., 173:273-276, 1991; Peace, D.J.; et al. (1991) J. Immunol., 146:2059-2065; Fenton, R.G.; et al. (1993) J. Natl. Cancer Inst., 85:1294-1302; Gedde-Dahl, T., III; et al. (1992) Hum. Immunol., 33:266-274, and Gedde-Dahl, T., III; et al. (1992) Int. Immunol., 4:1331-1337), the mutated Int6 proteins may elicit a specific T-cell

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° response via display on the tumor cell surface through the MHC apparatus.

The present invention therefore provides pharmaceutical compositions comprising Int6 protein or peptides derived therefrom for use in vaccines and in immunotherapy methods. When used as vaccines to protect mammals against cancer, the pharmaceutical composition can comprise as an immunogen cell lysate from cells transfected with a recombinant expression vector or a culture supernatant containing the expressed protein. Alternatively, the immunogen is a partially or substantially purified recombinant protein or a synthetic peptide.

—The above compositions or formulations, both for veterinary and for human use, comprise an immunogen as described above, together with one or more pharmaceutically acceptable carriers and optionally other therapeutic ingredients. The carrier(s) must be "acceptable" in the sense of being compatible with the other ingredients of the formulation and not deleterious to the recipient thereof. The formulations may conveniently be presented in unit dosage form and may be prepared by any method well-known in the pharmaceutical art.

All methods include the step of bringing into association the active ingredient with the carrier which constitutes one or more accessory ingredients. In general, the formulations are prepared by uniformly and intimately bringing into association the active ingredient with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product into the desired formulation.

Formulations suitable for intravenous intramuscular, subcutaneous, or intraperitoneal administration conveniently comprise sterile aqueous solutions of the active ingredient with solutions which are preferably

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° isotonic with the blood of the recipient. Such formulations may be conveniently prepared by dissolving solid active ingredient in water containing physiologically compatible substances such as sodium chloride (e.g. 0.1-2.0M), glycine, and the like, and
5 having a buffered pH compatible with physiological conditions to produce an aqueous solution, and rendering said solution sterile. These may be present in unit or multi-dose containers, for example, sealed ampoules or vials.

10 The formulations of the present invention may incorporate a stabilizer. Illustrative stabilizers are polyethylene glycol, proteins, saccharides, amino acids, inorganic acids, and organic acids which may be used either on their own or as admixtures. These stabilizers are
15 preferably incorporated in an amount of 0.11-10,000 parts by weight per part by weight of immunogen. If two or more stabilizers are to be used, their total amount is preferably within the range specified above. These stabilizers are used in aqueous solutions at the
20 appropriate concentration and pH. The specific osmotic pressure of such aqueous solutions is generally in the range of 0.1-3.0 osmoles, preferably in the range of 0.8-1.2. The pH of the aqueous solution is adjusted to be within the range of 5.0-9.0, preferably within the range
25 of 6-8. In formulating the immunogen of the present invention, anti-adsorption agent may be used.

Additional pharmaceutical methods may be employed to control the duration of action. Controlled release preparations may be achieved through the use of polymer to
30 complex or absorb the proteins or their derivatives. The controlled delivery may be exercised by selecting appropriate macromolecules (for example polyester, polyamino acids, polyvinyl, pyrrolidone, ethylenevinylacetate, methylcellulose,
35 carboxymethylcellulose, or protamine sulfate) and the con-

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centration of macromolecules as well as the methods of incorporation in order to control release. Another possible method to control the duration of action by controlled-release preparations is to incorporate the proteins, protein analogs or their functional derivatives, into particles of a polymeric material such as polyesters, polyamino acids, hydrogels, poly(lactic acid) or ethylene vinylacetate copolymers. Alternatively, instead of incorporating these agents into polymeric particles, it is possible to entrap these materials in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly(methylmethacrylate) microcapsules, respectively, or in colloidal drug delivery systems, for example, liposomes, albumin microspheres, microemulsions, nanoparticles, and nanocapsules or in macroemulsions.

When oral preparations are desired, the compositions may be combined with typical carriers, such as lactose, sucrose, starch, talc magnesium stearate, crystalline cellulose, methyl cellulose, carboxymethyl cellulose, glycerin, sodium alginate or gum arabic among others.

The proteins of the present invention may be supplied in the form of a kit, alone, or in the form of a pharmaceutical composition as described above.

Vaccination can be conducted by conventional methods. For example, the immunogen can be used in a suitable diluent such as saline or water, or complete or incomplete adjuvants. Further, the immunogen may or may not be bound to a carrier to make the protein immunogenic. Examples of such carrier molecules include but are not limited to bovine serum albumin (BSA), keyhole limpet hemocyanin (KLH), tetanus toxoid, and the like. The immunogen can be administered by any route appropriate for antibody production such as intravenous, intraperitoneal, intramuscular, subcutaneous, and the like. The immunogen

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may be administered once or at periodic intervals until a significant titer of anti-Int6 antibody is produced. The antibody may be detected in the serum using an immunoassay as described below.

In yet another embodiment, the present invention provides pharmaceutical compositions comprising nucleic acid sequence capable of directing host organism synthesis of an Int6 protein or of a peptide derived from the Int6 protein sequence. Such nucleic acid sequence may be inserted into a suitable expression vector by methods known to those skilled in the art. Expression vectors suitable for producing high efficiency gene transfer in vivo include, but are not limited to, retroviral, adenoviral and vaccinia viral vectors. Operational elements of such expression vectors are disclosed previously in the present specification and are known to one skilled in the art. Such expression vectors can be administered intravenously, intramuscularly, subcutaneously, intraperitoneally or orally.

Whether the immunogen is an Int6 protein, a peptide derived therefrom or a nucleic acid sequence capable of directing host organism synthesis of Int6 protein or peptides derived therefrom, the immunogen may be administered for either a prophylactic or therapeutic purpose. When provided prophylactically, the immunogen is provided in advance of the cancer or any symptom due to the cancer. The prophylactic administration of the immunogen serves to prevent or attenuate any subsequent onset of cancer. When provided therapeutically, the immunogen is provided at, or shortly after, the onset of cancer or any symptom associated with the cancer.

When the immunogen is a partially or substantially purified recombinant Int6 protein or an Int6 peptide, dosages effective to elicit an antibody response against Int6 range from about 10 μ g to about 1500 μ g.

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Dosages of *Int6* protein - encoding nucleic acid sequence effective to elicit an antibody response against *Int6* range from about 10 to about 1000 μ g.

The expression vectors containing a nucleic acid sequence capable of directing host organism synthesis of an *Int6* protein(s) may be supplied in the form of a kit, alone, or in the form of a pharmaceutical composition as described above.

The present invention further relates to a vaccine for immunizing a mammal against cancer comprising *Int6* protein or an expression vector capable of directing host organism synthesis of *Int6* protein in a pharmaceutically acceptable carrier.

In addition to use as vaccines and in immunotherapy, the above compositions can be used to prepare antibodies to *Int6* protein. To prepare antibodies, a host animal is immunized using the *Int6* protein or peptides derived therefrom or aforementioned expression vectors capable of expressing *Int6* protein or peptides derived therefrom. The host serum or plasma is collected following an appropriate time interval to provide a composition comprising antibodies reactive with the virus particle. The gamma globulin fraction or the IgG antibodies can be obtained, for example, by use of saturated ammonium sulfate or DEAE Sephadex, or other techniques known to those skilled in the art. The antibodies are substantially free of many of the adverse side effects which may be associated with other anti-viral agents such as drugs.

The antibody compositions can be made even more compatible with the host system by minimizing potential adverse immune system responses. This is accomplished by removing all or a portion of the Fc portion of a foreign species antibody or using an antibody of the same species as the host animal, for example, the use of antibodies from human/human hybridomas. Humanized antibodies (i.e.,

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nonimmunogenic in a human) may be produced, for example, by replacing an immunogenic portion of an antibody with a corresponding, but nonimmunogenic portion (i.e., chimeric antibodies). Such chimeric antibodies may contain the reactive or antigen binding portion of an antibody from one species and the Fc portion of an antibody (nonimmunogenic) from a different species. Examples of chimeric antibodies, include but are not limited to, non-human mammal-human chimeras, rodent-human chimeras, murine-human and rat-human chimeras (Robinson et al., International Patent Application 184,187; Taniguchi M., European Patent Application 171,496; Morrison et al., European Patent Application 173,494; Neuberger et al., PCT Application-WO 86/01533; Cabilly et al., 1987 Proc. Natl. Acad. Sci. USA 84:3439; Nishimura et al., 1987 Canc. Res. 47:999; Wood et al., 1985 Nature 314:446; Shaw et al., 1988 J. Natl. Cancer Inst. 80: 15553, all incorporated herein by reference).

General reviews of "humanized" chimeric antibodies are provided by Morrison S., 1985 Science 229:1202 and by Oi et al., 1986 BioTechniques 4:214.

Suitable "humanized" antibodies can be alternatively produced by CDR or CEA substitution (Jones et al., 1986 Nature 321:552; Verhoeyan et al., 1988 Science 239:1534; Biedler et al. 1988 J. Immunol. 141:4053, all incorporated herein by reference).

The antibodies or antigen binding fragments may also be produced by genetic engineering. The technology for expression of both heavy and light chain genes in E. coli is the subject the PCT patent applications; publication number WO 901443, WO901443, and WO 9014424 and in Huse et al., 1989 Science 246:1275-1281.

Alternatively, anti-Int6 antibodies can be induced by administering anti-idiotypic antibodies as immunogen. Conveniently, a purified anti-Int6 antibody preparation prepared as described above is used to induce anti-

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° idiotypic antibody in a host animal. The composition is administered to the host animal in a suitable diluent. Following administration, usually repeated administration, the host produces anti-idiotypic antibody. To eliminate an immunogenic response to the Fc region, antibodies produced by the same species as the host animal can be used or the Fc region of the administered antibodies can be removed. Following induction of anti-idiotypic antibody in the host animal, serum or plasma is removed to provide an antibody composition. The composition can be purified as described above for anti-Int6 antibodies, or by affinity chromatography using anti-Int6 antibodies bound to the affinity matrix. The anti-idiotypic antibodies produced are similar in conformation to the authentic Int6 antigen and may be used to prepare vaccine rather than using an Int protein.

15 When used as a means of inducing anti-Int6 antibodies in an animal, the manner of injecting the antibody is the same as for vaccination purposes, namely intramuscularly, intraperitoneally, subcutaneously or the like in an effective concentration in a physiologically suitable diluent with or without adjuvant. One or more booster injections may be desirable.

For both in vivo use of antibodies to Int6 proteins and anti-idiotypic antibodies and for diagnostic use, it may be preferable to use monoclonal antibodies.

25 Monoclonal anti-Int6 antibodies or anti-idiotypic antibodies can be produced by methods known to those skilled in the art. (Goding, J.W. 1983. Monoclonal Antibodies: Principles and Practice, Pladermic Press, Inc., NY, NY, pp. 56-97). To produce a human-human hybridoma, a human lymphocyte donor is selected. A donor known to have the Int6 antigen may serve as a suitable lymphocyte donor. Lymphocytes can be isolated from a peripheral blood sample or spleen cells may be used if the donor is subject to splenectomy. Epstein-Barr virus (EBV)

30 can be used to immortalize human lymphocytes or a human

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° fusion partner can be used to produce human-human hybridomas. Primary in vitro immunization with peptides can also be used in the generation of human monoclonal antibodies.

Antibodies secreted by the immortalized cells are
5 screened to determine the clones that secrete antibodies of the desired specificity. For monoclonal antibodies, the antibodies must bind to Int6 protein or peptide. For monoclonal anti-idiotypic antibodies, the antibodies must bind to anti-Int6 antibodies. Cells producing antibodies
10 of the desired specificity are selected.

The above described antibodies and antigen binding fragments thereof may be supplied in kit form alone, or as a pharmaceutical composition for in vivo use. When used as a pharmaceutical composition in immunotherapy, the
15 antibodies or chimeric antibodies described herein may also be coupled to toxin molecules, radioisotopes, and drugs by conventional methods (Vitetta et al. (1991) in "Biologic Therapy of Cancer" De Vita VT, Hellman S., Rosenberg, S.A. (eds) J.B. Lippincott Co. Philadelphia; Larson, S.M. et al. (1991) in "Biological Therapy of
20 Cancer" De Vita V.T., Hellman S., Rosenberg, S.A. (eds) J.B. Lippincott Co., Philadelphia). Examples of toxins to which the antibodies may be coupled to include, but are not limited to, Ricin and pseudomonas endotoxin. Examples
25 of drugs or chemotherapeutic agents include, but are not limited to, adriamycin. Examples of radioisotopes, include, but are not limited to, ¹³¹I. Antibodies covalently conjugated to the aforementioned agents can be used in cancer immunotherapy. The antibodies may also be
30 used as an immunoaffinity agent to purify Int6 proteins, for therapeutic uses, and for diagnostic use in immunoassays as described below.

The present invention therefore relates to a third method for detecting mutations of the Int6 gene
35 comprising:

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analyzing the protein of a subject for alterations in Int6 protein expression.

For analysis of protein by this method, protein is obtained from biological specimens such as tumor biopsy samples and the like. The protein can be obtained as a crude lysate or it can be further purified by methods known to one skilled in the art (Sambrook, J. et al. (1989) in "Molecular Cloning, A Laboratory Manual", Cold Spring Harbor press, Plainview, NY).

Crude protein lysate can be analyzed for Int6 protein by immunoassays using anti-Int6 antibody.

Immunoassays of the present invention may be a radioimmunoassay, Western blot assay, immunofluorescent assay, enzyme immunoassay, chemiluminescent assay, immunohistochemical assay and the like. Standard techniques known in the art for ELISA are described in Method in Immunodiagnosis, 2nd Edition, Rose and Bigazzi, eds., John Wiley and Sons, 1980 and Campbell et al., Methods of Immunology, W.A. Benjamin, Inc., 1964, both of which are incorporated herein by reference. Such assays may be a direct, indirect, competitive, or noncompetitive immunoassay as described in the art. (Oellerich, M. 1984. J. Clin. Chem. Clin. BioChem. 22:895-904).

Detection of the Int6 protein anti-Int6 antibody complex formed can be accomplished by reaction of the complex with a secondary antibody such as labelled anti-rabbit antibody. The label may be an enzyme which is detected by incubating the complex in the presence of a suitable fluorimetric or colorimetric reagent. Other detectable labels may also be used, such as radiolabels, or colloidal gold, and the like. The labelled Int6 protein-anti-Int6 antibody complex is then visualized by autoradiography.

The present invention also includes a method for treating cancer comprising administering pharmaceutical compositions comprising an Int6 protein, an expression

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vector containing nucleic acid sequence capable of directing host organism synthesis of an *Int6* protein, or anti-*Int6* antibody in a therapeutically effective amount. When provided therapeutically, the *Int6* protein, *Int6* protein-encoding expression vector or anti-*Int6* antibody coupled to radioisotopes, toxin molecules or drugs is provided at (or shortly after) the onset of infection or at the onset of any symptom of infection or disease caused by cancer. The therapeutic administration of the *Int6* protein, *Int6* protein-encoding expression vector, or anti-*Int6* antibody serves to attenuate the infection or disease.

The present invention also includes another method for treating a subject having cancer comprising:

- (a) immunizing a subject with an amount of *Int6* protein or an expression vector capable of directing host organism synthesis of *Int6* protein effective to elicit a specific T cell response;
- (b) isolating said T cells from said immunized subject; and
- (c) administering said T cells to said immunized subject or to an unimmunized subject in a therapeutically effective amount.

T cells populations reactive against the *Int6* protein may be isolated from a peripheral blood sample or spleen cells of a donor immunized with the *Int6* protein. Epstein-Barr virus (EBV) can be used to immortalize human lymphocytes or a human fusion partner can be used to produce human-human hybridomas. Primary in vitro immunization with *Int6* protein can also be used in the generation of T cells reactive to the *Int6* protein.

T cells are cultured for about 7 to about 90 days (Yanelli, J.R. J. Immunol. Methods 139:1-16 (1991)) and then screened to determine the clones of the desired

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- ° reactivity against the other peptide contained in the immunogenic chimeric protein using known methods of assaying T cell reactivity; T cells producing the desired reactivity are thus selected.

The above described T cells may be used for in vivo use as treatment for individuals afflicted with cancer by administering T cells to a mammal intravenously, intraperitoneally, intramuscularly or subcutaneously. Preferred routes of administration are intravenously or intraperitoneally.

10 The present invention also relates to a gene therapy method in which an expression vector containing a nucleic acid sequence representing the wild-type *Int6* gene is administered to a subject having a mutation of the *Int6* gene. A nucleic acid sequence representing wild-type *Int6*
15 gene is that shown in SEQ ID No. 1 and SEQ ID No:3. Such nucleic acid sequence may be inserted into a suitable expression vector by methods known to those skilled in the art. Expression vectors suitable for producing high efficiency gene transfer in vivo include retroviral,
20 adenoviral and vaccinia viral vectors.

Expression vectors containing a nucleic acid sequence representing wild-type *Int6* gene can be administered intravenously, intramuscularly, subcutaneously, intraperitoneally or orally. A preferred route of
25 administration is intravenously.

The invention also provides a diagnostic kit for detecting mutations of the *Int6* gene. This diagnostic kit comprises purified and isolated nucleic acid sequences useful as PCR primers in analyzing DNA or RNA for
30 mutations of the *Int6* disease gene.

Any articles or patents referenced herein are incorporated by reference. The following examples are presented to illustrate various aspects of the invention but are in no way intended to limit the scope thereof.

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ExamplesExample 1Identification of A Novel
Integration Site For The MMTV Genome

To identify new Int loci in mammary tumor DNAs that would not be biased by selective inbreeding for a high cancer phenotype, a feral mouse strain derived from a single breeding pair of *M. musculus* trapped in Czechoslovakia (CZECH II) (Gallahan, D. and Callahan, R. (1987) J. Virol, 61:66-74) was utilized. The CZECH II mice, unlike high-incidence inbred mouse strains, lack endogenous MMTV genomes but do contain an infectious strain of MMTV that is transmitted congenitally through the milk (Callahan, R. et al. (1982) Proc. Natl. Acad. Sci. U.S.A., 79:4113-4117). In the CZECH II mice, several preneoplastic hyperplastic outgrowth lines (HOGs) were developed which are stable, clonal-dominant and develop focal mammary tumors which sometimes metastasis to the lung. In order to detect the integration of MMTV proviral genome into genomic DNA of the HOGs or HOG-derived tumor or lung metastasis from a mouse having a HOG-derived tumor, cellular DNA was isolated from a CZECH II HOG line designated CZZ1 or from CZZ-1 derived malignant tumors or lung metastasis and analyzed by Southern blotting as follows. 10 ug of cellular DNA was digested by EcoRI, run on a 0.8% agarose gel, transferred to a nylon membrane and hybridized with MMTV LTR probe as described in Gallahan, D. and Callahan R. (J. Virol (1987) 61:66-74. In Brief, before hybridization, filters were soaked for 4 to 24 hours at 37° C in a prehybridization solution containing 3x SSPE (1x SSPE is 180 mM NaCl, 10 mM NaH₂PO₄ [pH 7.4], and 1 mM EDTA), 5x Denhardt solution (0.02% Ficoll, 0.02% polyvinylpyrrolidone, 0.02% bovine serum albumin), 2.5% dextran sulfate, and 50% formamide. Denatured probe was added to a solution similar to the prehybridization solution except that it contained 40% formamide. The

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° mixture was added to the plastic bag containing prehybridized filters and incubated at 37° C for 24 h. The filters were washed in stringent conditions involving three changes (each change done after 20 to 30 minutes of washing) of 0.1x SSC (1x SSC is 0.15 M NaCl plus 0.015 M sodium citrate) and 0.5% sodium dodecyl sulfate at 65° C. The filters were exposed to Kodak XAR-5 C-ray film overnight or for up to several days. The results of these Southern blots are shown in Figures 1A and 1B. The results presented in Figure 1A show that DNA from one CZZ-1 HOG line contained three MMTV proviral genomes (six EcoRI restriction fragments) integrated into the cellular DNA and that these proviral genomes were also present in primary tumors which arose independently from within the HOG. The results further demonstrated that CZZ-1 was clonal-dominant population of preneoplastic cells because these six MMTV-related fragments were reproducibly found in the original outgrowth and in each succeeding transplant generation. Indeed, the clonal-dominant nature of the CZZ-1 HOG is illustrated by tumor 1262 (lane 3, Figure 1A) in which one complete proviral genome, corresponding to the 4.8 and 2.8 Kb EcoRI restriction fragments, has been lost. The observation that five out of the thirteen tumor DNAs analyzed in Figure 1A and five out of eleven independent metastatic lesions in the lung of the mouse bearing tumor 4973 (Figure 1B) contained additional integrated MMTV genomes suggested that the additional integration events may have contributed to tumor progression by activating (or inactivating) additional cellular genes. However, since none of the known common insertions sites (*Wnt-1*, *Fgf-3*, *Int-3*, *Wnt-3*, and *Fgf-4*) were rearranged by MMTV in the CZZ-1 HOG, recombinant clones were obtained for each of the EcoRI host-MMTV junction restriction fragments in the CZZ-1 HOG and subclones of the host sequences were used as probes to screen Southern blots of independent MMTV-induced mammary

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- ° tumor DNAs for evidence of MMTV-induced DNA rearrangements.

Using this approach, a probe consisting of the host sequences flanking one of the MMTV proviruses in the CZZ-1 HOG (i.e., the 3.0 Kb fragment shown in Figure 1A) was used to identify an *Int6* common integration site in the CZZ-1 HOG derived tumor 22 (Figure 2A, lanes 2 and 3) and independent mammary tumors 1139 (Figure 2B, lanes 2 and 3) and 3144 (Figure 2C, lanes 2 and 3). In brief, cellular DNAs (10 μ g) from each tumor DNA and from normal liver DNA (lane 1 in each panel) were digested with *EcoRI*, run on a 0.8% agarose gel, and then blotted onto a nylon membrane. Lanes 1 and 2 of the blots in Figures 2A and 2B were hybridized with probe D which corresponds to host flanking sequences. Lane 2 of Figures 2A and 2B was subsequently hybridized with MMTV gag sequences (Gallahan and Callahan (1987) J. Virol., 61:66-74) and the results are shown in lane 3 of Figures 2A and 2B. Lanes 1 and 2 in Figure 2C were hybridized with probe C. Lane 2 was subsequently hybridized with MMTV env sequences (Gallahan and Callahan (1987) J. Virol., 61:66-74) and the result is shown in lane 3 of Figure 2C. Hybridizations of the respective blots with the first probe were carried out as described earlier in this Example (Gallahan and Callahan ((1987) J. Virol., 61:66-74)). Where blots were subsequently hybridized with a second probe, the blots were reprobed according to Gallahan and Callahan ((1987) J. Virol., 61:66-74) as follows. In brief, Genetran filters were stripped of probe DNA by placing the filters in 100 ml of 0.4 N NaOH and incubated for 20 minutes at room temperature. This solution was then discarded and replaced with 0.1 M Tris (pH 7.5)-0.1x SSC-0.5% sodium dodecyl sulfate solution to neutralize the filter. The filter was incubated for 15 minutes at room temperature, after which the neutralization solution was replaced and incubation was continued for another 15 minutes. The filter was then

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- ° prehybridized and hybridized as described earlier in this Example. Genetran filters treated in this way could be re-used at least five times before noticeable DNA loss.

The results show that MMTV-induced rearrangements (indicated by an arrow in Figures 2A-2C) were detected in the two independent MMTV-induced mammary tumor DNAs (lanes 2 and 3 of Figures 2B and 2C). Of interest, in each case where MMTV-induced rearrangements were detected, the rearranged restriction fragment co-migrated with a fragment containing either MMTV gag or env sequences. These results demonstrate that the transcriptional orientation of the viral genome in each tumor was in the same direction. Thus, the host sequences adjacent to the integrated MMTV genome define a new common integration site from MMTV designated *Int6*.

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Example 2

Isolation of the Murine *Int6* Gene

To obtain recombinant genomic clones of the *Int6* loci, a subclone of the 3.0 kb *EcoRI* fragment (shown in Figure 1A) containing the host flanking sequences (i.e. probe D, Figure 3) was used to probe a lambda phage library (Stratagene, LaJolla, CA) of genomic DNA from mouse strain 129/sv. This genomic DNA contains wild-type *Int6* DNA as determined by nucleotide sequence analysis. An additional three overlapping lambda clones which span 47 kb of the *Int6* locus have also been obtained using probes A-C (Figure 3). Together, these four overlapping lambda clones span the murine *Int6* gene as shown in Figure 3. The gene is located centromeric of the *myc* proto-oncogene on mouse chromosome 15. Further nucleotide sequence analysis of the genomic clones of the *Int6* locus demonstrated that the gene contains thirteen exons which span 34 Kb of genomic DNA as shown in Figure 3.

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Example 3Expression of the Int6 Gene In CZECH II Mammary Tumors

To examine Int6 expression in CZECH II mammary tumors, total RNA (20 µg) prepared from the Int6 negative tumor (tumor 178) and from Int6 positive tumors having viral insertions in Int6 (22 and 1139) was denatured in the presence of formaldehyde and run on a 1% agarose gel containing formaldehyde. The RNA was then transferred to a nylon membrane and hybridized with probe A (Figure 3) as described in Gallahan, D. and Callahan, R. (1987) J. Virol., 61:66-74. The results of the Northern blots are shown in Figure 4. In brief, hybridization with probe A detected a 1.4 Kb species of RNA in each of three tumors and tumor 1139 also contained a 0.9 Kb species of RNA related to sequences in probe A. The observation that tumor 178 (Figure 4) and several other MMTV induced mammary tumors in which Int6 is not rearranged by the virus expressed the 1.4 kb RNA species detected by probe A. This suggests that in tumors 22 and 1139 the level of the Int6 gene expression is not an important consequence of viral integration in this locus.

Example 4Isolation of Wild-Type Murine Int6 cDNA

In order to isolate a cDNA corresponding to wild-type 1.4 kb Int6 RNA, a murine cDNA library of an MMTV induced mammary tumor in which Int6 was not rearranged by MMTV was prepared using standard techniques (Sambrook et al (1989) in "Molecular Cloning, A Laboratory Manual", Cold Spring Harbor Press, Plainview NY) and was probed with probe A (probe A is the XbaI fragment shown in Figure 3). The nucleotide sequence of the murine Int6 cDNA was determined and is shown in Figure 5. Translation of the 1.4 kb species of Int6 RNA revealed an open reading frame which encodes a 43.5 kilodalton protein. As shown in Figure 5, this protein contains two potential N-glycosylation site

motifs (Gavel, Y. and von Heijne, G. (1990) Protein Eng., 3:433-442) as well as potential phosphorylation site motifs for cyclic AMP/cyclic GMP-dependent protein kinase (Glass, D.B. et al (1986) J. Biol. Chem., 261:2987-2993), protein kinase C (Kishimoto, A. et al (1985) J. Biol. Chem., 260:12492-12499), tyrosine kinases (Hunter, T. and Cooper, J.A. (1985) Ann. Rev. Biochem., 54:897-930) and casein kinase II (Pinna, L.A. (1990) Biochim Biophys Acta, 1054:267-284).

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Since all of the genes whose expression has been affected or altered by MMTV integration in mouse mammary tumors have been highly conserved through evolution (Dickson, C. and Peters, G. (1987) Nature 326:883; Rijsewizk, K.F. et al (1987) Cell, 50:649-657; Robbins, J. et al (1992) J. Virol., 66:2594-2599), the conservation of the *Int6* gene in genomic DNA of different species was examined via Southern blot analysis. Cellular DNAs (10 μ g each) from *C. elegans*, *Drosophila*, *Xenopus*, chicken, mouse, and human were digested with BamHI, run on a 0.8% agarose gel, transferred to a nylon membrane and hybridized overnite with *Int6* cDNA in 3x SSPE (1x SSPE is 180mM BaCl, 10 mMNaH₂PO₄[pH 7.4, and 1 mM EDTA), 5x Denhardt solution (0.02% Ficoll, 0.02% polyvinylpyrrolidone, 0.02% bovine serum albumin), 5% dextran sulfate and 2% SDS (sodium dodecyl sulfate) at 65°C. After hybridization, the blot was washed in stringent condition involving three changes (each change done after 20 to 30 minutes of washing) 0.5x SSC (1x SSC is 0.15 M NaCl plus 0.015 M sodium citrate) plus 0.5% SDS at 65°C. Exposure to Kodak XAR-5 film was for three days. As shown in Figure 6, *Int6* related sequences can be detected in all the eukaryotic species examined. Restriction fragments of yeast DNA which contain *Int6*

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° related sequences were also detected by Southern blot analysis (data not shown).

In addition, the nucleotide sequence of a cDNA clone of the Drosophila homolog of Int6 has been determined (data not shown) and the deduced amino acid sequence of the Drosophila Int6 protein is 60% identical to the human/mouse deduced amino acid sequences. Taken together, these results demonstrate an extensive evolutionary conservation of the Int6 gene which is indicative of Int6 serving a basic life function.

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Example 6

Detection of Int6-specific mRNA Expression in Target Tissues

Having detected the 1.4 Kb Int6 RNA species in a tumor in which the gene was not rearranged by MMTV (i.e., tumor 178, Figure 4) normal adult tissues and embryos at different stages of development were surveyed for Int6 RNA expression via Northern analysis as follows. Total RNAs (10 µg each) was prepared from the indicated tissues. The RNAs were denatured in the presence of formaldehyde and run on 1% agarose gels containing formaldehyde. The RNA samples were then transferred to a nylon membrane and hybridized sequentially with a β -actin probe and then an Int6 cDNA probe under conditions described in Gallahan and Callahan (J. Virol., 61:66-74 (1987)). As shown in Figure 7, Int6 RNA is expressed in all adult tissues tested, including the mammary gland, and expression of Int6 RNA in embryos was detected as early as day eight of development.

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Example 7

Detection of Int6-specific mRNA Expression in Target Tissues

To detect Int6-specific mRNA expression, Random primed cDNA is prepared using total RNA from the various tissues. A 700 bp fragment of Int6 murine cDNA is

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- ° amplified by PCR using the primers shown as SEQ ID NO.29
TGTCCACATATTCTACGCTA and SEQ ID NO. 30
TGTATGTCATCCTTTATACA. The conditions of the PCR are: 30
cycles of denaturation at 94°C for 1 minute, annealing at
55°C for 1 minute, and extension at 72°C for 2 minutes.
5 After the last cycle there is an additional extension time
of 2 minutes. The PCR product is run on a 1.0% agarose
gel. The RT-PCR products are detected by photographing
the gel following staining with ethidium bromide.

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Example 8

Rearrangement of *Int6* by MMTV
Leads to the Expression of Novel
Species of *Int6* RNA in Mammary Tumors

- Inspection of the mapping data for the murine *Int6*
gene as shown in Figure 3 reveals that all of the viral
15 integration events occur within introns of the *Int6* gene
and that the transcriptional direction of the integrated
viral genome is in the opposite orientation to that of the
Int6 gene. There are at least four possible scenarios for
the role MMTV plays at the *Int6* locus. In the first, the
20 *Int6* gene is in fact not the target gene on which MMTV
acts. At the *Wnt1*, *Fgf-3*, and *Fgf-4* loci (Dickson, C., et
al. (1984) Cell. 37:529-536; Nusse, R., et al. (1982)
Cell. 31:99-109; Peters, G., et al. (1989) Proc. Natl.
Acad. Sci. USA. 86:5678-5682), MMTV integration sites
25 cluster around the target gene in an ordered fashion and
the transcriptional orientation of the integrated viral
genomes 5' of the target gene are in the opposite
direction to that of the target gene whereas those 3' of
the target gene are in the same transcriptional
30 orientation. Further, based on published reports, MMTV
integration sites are within 15 kb of the particular
target gene. However, since no evidence was found for the
activation of expression of RNA corresponding to sequences
up to 13 kb 3' of the *Int6* gene, the location of the

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- 50 -

putative target gene would have to be more than 24 kb from the integrated MMTV genome in CZZ-1 HOG and more than 30 kb in tumor 1139 (see Figure 3), thereby making this possibility much less likely.

A second possible consequence of MMTV integration into the *Int6* gene is the activation of expression of a new chimeric RNA transcript of *Int6* initiated by the 3' LTR of the integrated viral genome. An analogous situation occurs in MMTV-induced rearrangements of *Int-3* (Robbins, J., et al. (1992) J. Virol., 66:2594-2599) except in the case of *Int6*, this would result in the expression of *Int6* anti-sense RNA since the transcriptional orientation of the viral genome is opposite to that of *Int6*. Such a result would represent a trans-dominant mutation that would inactivate the expression of both alleles. However, using a variety of techniques, MMTV-induced *Int6* antisense RNA expression has not been detected.

A third possibility assumes that the *Int6* gene is the target for MMTV integration within the *Int6* locus. In this case the viral insertion would disrupt the expression of one allele and reveal the presence of a spontaneous recessive mutation in the other allele. To examine this possibility the nucleotide sequence of cDNA corresponding to the non-rearranged allele of *Int6* in tumor 22 and tumor 1139 was determined and in both cases no mutation was found.

The fourth and more plausible scenario is that MMTV integration into the *Int6* gene causes the expression of a biologically activated gene product (like *Int3*, (Robbins, J., et al. (1992) J. Virol., 66:2594-2599)) or a dominant-negative gene product either of which deregulates the normal control of mammary epithelial cellular growth leading to hyperplasia of the affected mammary epithelial cells. This would create a premalignant epithelial cell

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- ° population with which mammary tumors could subsequently develop.

To test whether integration of MMTV into the *Int6* gene produces altered RNA species, the nucleotide sequence of cDNA clones of *Int6* RNA from tumor 1139 and tumor 22. In each case transcription of the rearranged allele resulted in the expression of a chimeric RNA species which terminated at a cryptic transcription stop signal in the reverse U3 portion of the MMTV LTR (Figure 8). Of interest, a similar cryptic transcription termination signal has previously been shown to be active in certain MMTV induced rearrangements *Fgf-3* (Clausse, N., (1993) Virology, 194:157-165).

Figures 9A and 9B show the nucleotide-sequences of *Int6*-MMTV LTR RNA species detected in tumors 1139 (Figure 9A) and 22 (Figure 9B). In Figure 9A, two RNA species from the rearranged allele (Figure A, 900 bp and 965 bp) were detected. The RNA species correspond to the 900 bp RNA species detected by Northern blot analysis in Figure 4. In one RNA species exon 5 was spliced to the end of the U5 portion of the MMTV LTR and in the other species splicing occurred at a cryptic splice acceptor site in intron 5. Similarly, Figure 9B, CZZ-1 there were three chimeric RNA species in which exon 9 was spliced to one of three different cryptic splice acceptor sites in intron 9. Since the size of the chimeric tumor RNA species is similar to that of the normal *Int6* RNA, they went undetected in the Northern blot analysis of tumor 22 RNA Figure 4.

Translation of the rearranged *Int6* RNA species into putative proteins revealed that from all five species, the product is a truncated chimera of the *Int6* amino acid sequences linked to novel amino acid sequences encoded by an *Int6* intron and/or reverse MMTV LTR nucleotide sequences. The presence of the 965 bp RNA species in

- 52 -

tumor 1139 suggests that truncation of the *Int6* gene product is an important consequence of MMTV integration.

Example 9

Isolation Of The Human *Int6* Gene

5 Mouse *Int6* cDNA was used to probe a cDNA library of human lung RNA in lambda phage (Clontech Inc.) and using primers specific for the human *Int6* cDNA (SEQ ID NO:3) cloned from the human lung cDNA library, a P1 phage library of human genomic DNA was screened by PCR for an
10 *Int6*-related clone by Genome Systems Inc. (St. Louis, MO). Using this approach, a P1 phage clone and two lambda clones containing over 50 kb of human genomic DNA were obtained. Nucleotide sequence analysis of these clones revealed that the human *Int6* gene is organized as shown in
15 Figure 10. As in the mouse genome, the human *Int6* gene is composed of 13 exons. The human *Int6* gene also contains a CA-repeat sequence in the seventh intron (Figure 10).

Example 10

Size Polymorphism Of The CA Repeat Sequence Contained In Intron 7

20 Primers complementary to the nucleic acid sequences flanking the CA-repeat in intron 7 of the human *Int6* gene (Figure 1) and having the sequences shown in SEQ ID NO:31
25 1³ GTGAAAATGACATGAAATTTTCAG and SEQ ID NO:32
2⁴ TGCAGTGTGACAATATGGGC were used to PCR amplify the portion of the *Int6* gene containing the CA-repeat in human genomic DNA. The conditions of the PCR were: 30 cycles of denaturation at 94°C for one minute, annealing at 55°C for one minute, and extension at 72°C for two minutes. After
30 the last cycle, there was an additional extension time of two minutes. Separation of the PCR products via non-denaturing 6% polyacrylamide gel electrophoresis revealed that 46 of the 84 individual DNAs analyzed were
35 heterozygous (informative) for different size alleles.

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Example 11Chromosomal Localization Of The Human Int 6 Gene

To determine the chromosomal localization of the human *Int6* gene, Southern blot analysis of human DNA and DNA isolated from rodent-human somatic cell hybrids containing individual human chromosomes was performed. In brief, rodent-human somatic cell hybrid DNA or human DNA was digested with HindIII and hybridized with human *Int6* cDNA at 37°C for 24 hours in 3x SSPE, 5X Denhardt solution, 2.5% dextran sulfate and 40% formamide. The blot was then washed under stringent conditions involving three changes (each change done after twenty to thirty minutes) of 0.1x SSC and 0.5% SDS at 65°C. The results of this Southern blot are shown in Figure 12 where lanes 1 and 2 contain Chinese hamster-human somatic cell hybrid DNA containing human chromosome 6 (lane 1) or 8 (lane 2), lane 3 contains DNA from mouse-human somatic cell hybrids containing human chromosomes 3, 7, 8, 15 and 17 and lane 4 contains human genomic DNA. The 23 kb fragment shown in lane 4 contains an *Int6*-related pseudogene and the coding sequences of the *Int6* gene are defined by the 4.5, 3.5 and 3.0 kb fragments shown in lane 4. The results show that while the 23 kb fragment was detected only in lane 1 (hybrids containing human chromosome 6), the 4.5 and 3.5 kb fragments were detected in lane 2 (hybrids containing human chromosome 8). In addition, the 3.0 kb human fragment (see lane 4) was also detected in both lanes 1 and 2. However, the detection of the 3.0 kb fragment in lane 3 confirmed that the 3.0 kb fragment contains human *Int6*-related sequence rather than Chinese hamster sequence since mouse DNA was shown not to contain an *Int6*-related 3.0 kb Hind III fragment. These results demonstrate that the human *Int6* gene is located on chromosome 8. This chromosomal localization was confirmed and further refined to chromosome 8q22-q24 by linkage analysis using the CA-repeat polymorphism described in Example 10.

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Example 12Detection Of Mutations In The Int6 Gene In Human Breast Tumor DNA Resulting In A Loss Of Heterozygosity

Based on the results in MMTV-induced mouse mammary tumors presented earlier, DNA from human breast cancer biopsies was analyzed to determine whether the Int6 gene might be a target for mutation during malignant progression in human breast cancer. In brief, DNA from primary human breast tumor and from matching normal tissue of 40 individuals that were informative at the Int6 CA-repeat sequence were analyzed for evidence of loss of heterozygosity (LOH) in the tumor DNA via the PCR method utilized in Example 10. In eleven of these tumors (25%), there was either a complete loss or a significantly reduced signal of one allele relative to the matching normal DNA. Five of these eleven tumor DNAs (T) and their matching normal samples (L) are shown in Figure 13. These results show that Int6 is a target for mutation during malignant progression in human breast cancer. Further, since Int6 gene expression has been detected in all tissues analyzed (see Figure 7), mutation of the Int6 gene may occur during progression of cancers found in other tissues.

Example 13Analysis Of The Human Int6 Gene for Mutations By PCR-SSCP Using Primer Pairs Derived From Sequences Bounding Exons Of The Int6 Gene

Primer pairs complementary to nucleic acid sequences bounding 12 of the 13 human Int6 exons (Figure 14) are shown as SEQ ID NOs:5-28. Using primer pairs selected from SEQ ID NOs:5-28, each of the exons of the Int6 gene except exon 7 were amplified from the eleven primary breast tumor DNAs having loss of heterozygosity at the Int6 gene (see Example 12) and from DNA of matching normal tissue samples by PCR and the PCR products were analyzed for single-stranded conformation polymorphism (SSCP) via

- 55 -

denaturing polyacrylamide gel electrophoresis. Exon 7 was analyzed by hybrid mismatch methodology using the portion of human Int6 cDNA corresponding to exon 7. Analysis by both single strand conformation polymorphism analysis (SSCP) and hybrid mismatch methodologies of the primary breast tumor DNAs having loss of heterozygosity at the Int6 gene detected no point mutations in the remaining allele (data not shown). However, the promoter and intron regions of the remaining allele were not analyzed for mutations. Of course, if mutations of the promoter, intron and/or coding regions of the Int6 gene were detected in tumor samples, these mutations could be confirmed by nucleotide sequence analysis of the variant allele in the tumor and matching normal tissue DNA.

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Example 14Loss of Expression of Int6 mRNA
In Human Breast and Lung Tumor Samples

Total RNA isolated from 36 malignant human breast tumors, 2 preneoplastic lesions (high grade dysplasia) and matching normal tissue were surveyed for Int6 mRNA expression via Northern blot analysis using sequential hybridization with β -actin and human Int6 cDNA probes under conditions described in Gallahan and Callahan (J. Virol. 61:66-74 (1987)). Of these 38 samples, 14 (37%) exhibited significantly reduced or nondetectable Int6 mRNA expression as compared with matching normal tissue samples.

25

Of these 14 cases, 8 were invasive ductal carcinomas (IDC), 2 were comedocarcinomas (IDC with a prevalent intraductal component), 2 were lobular carcinomas and 2 were the preneoplastic lesions. A representative Northern blot is shown in Figure 15.

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In a separate study, Int6 mRNA expression in 47 nonsmall cell lung carcinomas (NSCLC) and matching normal tissues was surveyed via Northern analysis of 10 μ g total

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RNA as described above in this Example. A representative Northern blot is shown in Figure 16 and the results of the Northern analyses of the 47 NSCLC samples are summarized in Table 1.

TABLE 1

ASSOCIATIONS BETWEEN LOSS OF EXPRESSION
OF *Int6* AND CLINICAL PARAMETERS

| | HISTOTYPE | REDUCED OR NONDETECTABLE EXPRESSION | NORMAL EXPRESSION | TOTAL SAMPLES | P VALUE |
|----|--------------------|---|----------------------|------------------|---------|
| 10 | SQUAMOUS CELL | 3(14%) | 18 | 21 | |
| | ADENOCARCINOMA | 8(67%) | 4 | 12 | 0.003 |
| | BRONCHIOLOALVEOLAR | 2(33%) | 4 | 6 | |

Of interest, 14 of 47 NSCLCs showed loss of *Int6* mRNA expression and loss of *Int6* mRNA expression was observed to have a highly significant association ($P = 0.003$) with a particular histologic subtype (Table 1, adenocarcinoma of NSCLC).

The results presented in this Example are consistent with the conclusion that loss of *Int6* expression is an early event in human breast cancer and a contributing factor in other neoplasias such as those of the lung.

Example 15

Characterization of the Murine *Int6* Protein

The *Int6* gene encodes a 50 kD protein with three potential translation start sites (at 27 bp, 174 bp and 189 bp of the mouse sequence). Each of these polypeptides were detected as products of in vitro translation of *Int6* RNA in the rabbit reticulocyte system. Rabbit polyclonal sera to synthetic peptides corresponding to amino acid residues 57-71 (peptide 47) and 262-281 (peptide 20) of mouse *Int6* were prepared and used to immunoprecipitate the

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° Int6 in vitro translation products. This immunoprecipitation was competed by the corresponding peptide. Western blot analysis of protein extracts of adult mouse tissues (brain, lung, kidney, muscle, heart and mammary gland), using antibodies to peptide 20 (rAB 20), detected a major 40KD polypeptide as well as a triplet of 80 KD polypeptides. Reaction with these polypeptides was competed with peptide 20. Of interest, expression of a 30 KD Int6 related polypeptide was also observed in Western blots of salivary gland extracts. It is believed that the 40KD polypeptide may represent a cleavage product of the 50KD precursor and that the 80KD cross reacting polypeptide may represent dimers of the 40KD polypeptides.

In addition, cell fractionation studies and immunofluorescence studies using antibodies to the above peptides have demonstrated that Int6 is primarily localized to the cytoplasm. Moreover, in immunofluorescence studies of mouse embryos, the Int6 protein was localized to the golgi apparatus.

Finally, Int6 protein, which contains three candidate protein kinase C (PKC) phosphorylation sites, was expressed in bacteria using the QUIA Express Type 4 vector (Quiagen, Chatsworth CA), purified and shown to be phosphorylated by PKC (data not shown).

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30

35

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANTS: The Government of the United States of America as represented by the Secretary, Department of Health and Human Services; Callahan, Robert; Marchetti, Antonio; Buttitta, Fiamma; Smith, Gilbert H.
- 10 (ii) TITLE OF INVENTION: Nucleotide And Deduced Amino Acid Sequences Of A New Tumor Gene, Int6, And the Use Of Reagents Derived From These Sequences In Diagnostic Assays, Vaccines, Immunotherapy And Gene Therapy
- (iii) NUMBER OF SEQUENCES: 32
- 15 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
(B) STREET: 345 PARK AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: USA
(F) ZIP: 10154
- 20 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: FLOPPY DISK
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WORDPERFECT 5.1
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 09-FEB-1996
(C) CLASSIFICATION:
- 25 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/385,998
(B) FILING DATE: 09-FEB-1995
(C) CLASSIFICATION:
- 30 (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: William S. Feiler
(B) REGISTRATION NUMBER: 26,728
(C) REFERENCE/DOCKET NUMBER: 2026-4179PCT
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 758-4800
(B) TELEFAX: (212) 751-6849
(C) TELEX: 421792
- 35

- 59 -

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1504 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:1:

| | | | | | |
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| | AACAAGCGCT | CCTTTCCCCC | GGCAAGATGG | CGGAGTACGA | 40 |
| | CCTGACTACT | GCATCGCGCA | TTTTCTGGAT | CGGCACCTGG | 80 |
| | TCTTTCCGCT | TCTTGAGTTT | CTCTCTGTGA | AAGAGATTTA | 120 |
| | TAATGAAAAA | GAATTATTAC | AAGGAAAATT | AGATCTTCTT | 160 |
| | AGTGATACCA | ATATGGTGGG | CTTTGCTATG | GATGTTTACA | 200 |
| 10 | AAAACCTTTA | TTCTGATGAT | ATCCCTCATG | CTTTGAGAGA | 240 |
| | AAAAAGAACC | ACAGTTGTTG | CGCAGCTGAA | ACAGCTCCAG | 280 |
| | GCAGAAACAG | AACCAATTGT | GAAGATGTTT | GAAGATCCAG | 320 |
| | AAACTACAAG | GCAGATGCAG | TCAACCAGGG | ATGGCAGGAT | 360 |
| | GTTATTTGAC | TACCTGGCAG | ACAAACATGG | GTTTAGGCAA | 400 |
| | GAGTACTTAG | ATACACTCTA | CAGATACGCA | AAATTCCAGT | 440 |
| | ATGAGTGTGG | AAATTACTCT | GGAGCTGCAG | AGTATCTTTA | 480 |
| | CTTCTTTAGA | GTTTGTGGTCC | CAGCAACAGA | TAGAAATGCT | 520 |
| 15 | TTAAGTTCGC | TCTGGGGAAA | ACTGGCCTCT | GAAATCTTAA | 560 |
| | TGCAGAATTG | GGATGCAGCC | ATGGAAGACC | TTACTCGATT | 600 |
| | AAAAGAAACC | ATAGACAATA | ATTCTGTGAG | TTCTCCACTC | 640 |
| | CAGTCTCTTC | AGCAGCGAAC | ATGGCTCATT | CATTGGTCTC | 680 |
| | TATTTGTTTT | TTTCAACCAT | CCAAAGGGCC | GTGATAACAT | 720 |
| | TATTGATCTC | TTCCTTTACC | AACCACAGTA | TCTTAATGCA | 760 |
| | ATTCAGACAA | TGTGTCCACA | TATTCTACGC | TATTTGACTA | 800 |
| 20 | CTGCCGTCAT | AACCAACAAA | GATGTGCGGA | AACGCCGGCA | 840 |
| | GGTGCTGAAA | GATCTGGTGA | AAGTGATTCA | ACAGGAGTCT | 880 |
| | TACACATATA | AAGACCCAAT | TACAGAATTT | GTTGAATGCC | 920 |
| | TATATGTTAA | CTTTGATTTT | GACGGGGCTC | AGAAAAAGCT | 960 |
| | GAGAGAATGT | GAATCAGTGC | TCGTGAATGA | CTTCTTCCTG | 1000 |
| | GTAGCGTGTC | TGGAGGACTT | CATTGAGAAT | GCCCGTCTCT | 1040 |
| | TCATATTTGA | GACGTTTTGT | CGTATCCACC | AGTGATCAG | 1080 |
| 25 | CATTAATATG | TTAGCAGATA | AACTGAATAT | GACTCCAGAA | 1120 |
| | GAAGCTGAAA | GATGGATTGT | GAATTTGATT | AGAAATGCCA | 1160 |
| | GGTTGGATGC | CAAGATTGAT | TCTAAACTAG | GTCATGTGGT | 1200 |
| | AATGGGCAAC | AATGCAGTCT | CGCCCTACCA | GCAAGTGATT | 1240 |
| | GAAAAGACCA | AAAGCCTTTC | TTTTAGAAGC | CAAATGTTGG | 1280 |
| | CCATGAATAT | TGAAAAGAAA | CTTAATCAGA | ACAGTAGATC | 1320 |
| | AGAGGCTCCC | AACTGGGCAA | CCCAAGACTC | TGGCTTCTAT | 1360 |
| | TAAAGGATTA | TAAAGAAAAG | AAGAAAAAGG | AATAAGTGAA | 1400 |
| 30 | AGACACAGTA | GCCATTGTGT | ATAAAGGATG | ACATACATTT | 1440 |
| | TTAGAAGCAA | TTAACATGTT | TGCTACAAAT | TTTGGAGAAT | 1480 |
| | TTGAATAAAA | TTGGCTATGA | TTAA | | 1504 |

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 396 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

[illegible]

- 61 -

| | | | | | | | | | | | | |
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| 0 | Val | Ala | Cys | Leu | Glu | Asp | Phe | Ile | Glu | Asn | Ala | Arg |
| | | | | 280 | | | | | 285 | | | |
| | Leu | Phe | Ile | Phe | Glu | Thr | Phe | Cys | Arg | Ile | His | Gln |
| | | 290 | | | | | 295 | | | | | 300 |
| | Cys | Ile | Ser | Ile | Asn | Met | Leu | Ala | Asp | Lys | Leu | Asn |
| | | | | | 305 | | | | | 310 | | |
| | Met | Thr | Pro | Glu | Glu | Ala | Glu | Arg | Trp | Ile | Val | Asn |
| | | | | | | | | 320 | | | | |
| 5 | Leu | Ile | Arg | Asn | Ala | Arg | Leu | Asp | Ala | Lys | Ile | Asp |
| | 325 | | | | | 330 | | | | | | 335 |
| | Ser | Lys | Leu | Gly | His | Val | Val | Met | Gly | Asn | Asn | Ala |
| | | | | 340 | | | | | 345 | | | |
| | Val | Ser | Pro | Tyr | Gln | Gln | Val | Ile | Glu | Lys | Thr | Lys |
| | | 350 | | | | | 355 | | | | | 360 |
| | Ser | Leu | Ser | Phe | Arg | Ser | Gln | Met | Leu | Ala | Met | Asn |
| | | | | | 365 | | | | | 370 | | |
| 10 | Ile | Glu | Lys | Lys | Leu | Asn | Gln | Asn | Ser | Arg | Ser | Glu |
| | | | 375 | | | | | 380 | | | | |
| | Ala | Pro | Asn | Trp | Ala | Thr | Gln | Asp | Ser | Gly | Phe | Tyr |
| | 385 | | | | | 390 | | | | | | 395 |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:3:

| | | | | | |
|----|-------------|------------|------------|------------|-----|
| | ACTCCCTTTT | CTTTGGCAAG | ATGGCGGAGT | ACGACTTGAC | 40 |
| | TACTCGCATC | GCGCACTTTT | TGGATCGGCA | TCTAGTCTTT | 80 |
| | CCGCTTCTTG | AATTTCTCTC | TGTAAAGGAG | ATATATAATG | 120 |
| | AAAAGGAATT | ATTACAAGGT | AAATTGGACC | TTCTTAGTGA | 160 |
| | TACCAACATG | GTAGACTTTG | CTATGGATGT | ATACAAAAAC | 200 |
| 25 | CTTTATTCTG | ATGATATTCC | TCATGCTTTG | AGAGAGAAAA | 240 |
| | GAACCACAGT | GGTTGCACAA | CTGAAACAGC | TTCAGGCAGA | 280 |
| | AACAGAACCA | ATTGTGAAGA | TGTTTGAAGA | TCCAGAAACT | 320 |
| | ACAAGGCAA | TGCAGTCAAC | CAGGGATGGT | AGGATGCTCT | 360 |
| | TTGACTACCT | GGCGGACAAG | CATGGTTTTA | GGCAGGAATA | 400 |
| | TTTAGATACA | CTCTACAGAT | ATGCAAAATT | CCAGTACGAA | 440 |
| | TGTGGGAATT | ACTCAGGAGC | AGCAGAATAT | CTTTATTTTT | 480 |
| 30 | TTAGAGTGCT | GGTTCCAGCA | ACAGATAGAA | ATGCTTTAAG | 520 |
| | TTCACTCTGG | GGAAAGCTGG | CCTCTGAAAT | CTTAATGCAG | 560 |
| | AATTGGGATG | CAGCCATGGA | AGACCTTACA | CGGTTAAAG | 600 |
| | AGACCATAGA | TAATAATTCT | GTGAGTTCTC | CACCTCAGTC | 640 |
| | TCTTTCAGCAG | AGAACATGGC | TCATTCACTG | GTCTCTGTTT | 680 |
| | GTTTTCTTCA | ATCACCCCAA | AGGTCGCGAT | AATATTATTG | 720 |
| | ACCTCTTCCT | TTATCAGCCA | CAATATCTTA | ATGCAATTCA | 760 |
| | GACAATGTGT | CCACACATTC | TTCGCTATTT | GACTACAGCA | 800 |
| | GTCATAACAA | ACAAGGATGT | TCGAAAACGT | CGGCAGGTTT | 840 |

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| | | | | | |
|----|------------|-------------|------------|------------|------|
| 0 | TAAAAGATCT | AGTTAAAGTT | ATTCAACAGG | AGTCTTACAC | 880 |
| | ATATAAAGAC | CCAATTACAG | AATTTGTTGA | ATGTTTATAT | 920 |
| | GTAACTTTG | ACTTTGATGG | GGCTCAGAAA | AAGCTGAGGG | 960 |
| | AATGTGAATC | AGTGCTTGTG | AATGACTTCT | TCTTGGTGGC | 1000 |
| | TTGTCTTGAG | GATTTTCATTG | AAAATGCCCG | TCTCTTCATA | 1040 |
| | TTTGAGACTT | TCTGTGCGCAT | CCACCAGTGT | ATCAGCATT | 1080 |
| | ACATGTTGGC | AGATAAATTG | AACATGACTC | CAGAAGAAGC | 1120 |
| 5 | TGAAAGGTGG | ATTGTAAATT | TGATTAGAAA | TGCAAGACTG | 1160 |
| | GATGCCAAGA | TTGATTCTAA | ATTAGGTCAT | GTGGTTATGG | 1200 |
| | GTAACAATGC | AGTCTCACCC | TATCAGCAAG | TGATTGAAAA | 1240 |
| | GACCAAAAGC | CTTTCCTTTA | GAAGCCAGAT | GTTGGCCATG | 1280 |
| | AATATTGAGA | AGAAACTTAA | TCAGAATAGC | AGGTCAGAGG | 1320 |
| | CTCCTAACTG | GGCAACTCAA | GATTCTGGCT | TCTACTGAAG | 1360 |
| | AACCATAAAG | AAAAGATGAA | AAAAAAACT | ATCAAAGAAA | 1400 |
| | GATGAAATAA | TAAACTATT | ATATAAAGGG | TGACTTACAT | 1440 |
| 10 | TTTGGAACA | ACATATTACG | TATAAATTTT | GAAGAATTGG | 1480 |
| | AATAAAATTG | ATTCATTTTA | | | 1500 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 396 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:4:

| | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 20 | Met | Val | Asp | Phe | Ala | Met | Asp | Val | Tyr | Lys | Asn | Leu |
| | 1 | | | | 5 | | | | | 10 | | |
| | Tyr | Ser | Asp | Asp | Ile | Pro | His | Ala | Leu | Arg | Glu | Lys |
| | | | 15 | | | | | 20 | | | | |
| | Arg | Thr | Thr | Val | Val | Ala | Gln | Leu | Lys | Gln | Leu | Gln |
| | 25 | | | | 30 | | | | | 35 | | |
| | Ala | Glu | Thr | Glu | Pro | Ile | Val | Lys | Met | Phe | Glu | Asp |
| | | | 40 | | | | | 45 | | | | |
| 25 | Pro | Glu | Thr | Thr | Arg | Gln | Met | Gln | Ser | Thr | Arg | Asp |
| | 50 | | | | 55 | | | | | | 60 | |
| | Gly | Arg | Met | Leu | Phe | Asp | Tyr | Leu | Ala | Asp | Lys | His |
| | | | 65 | | | | | 70 | | | | |
| | Gly | Phe | Arg | Gln | Glu | Tyr | Leu | Asp | Thr | Leu | Tyr | Arg |
| | | 75 | | | | 80 | | | | | | |
| | Tyr | Ala | Lys | Phe | Gln | Tyr | Glu | Cys | Gly | Asn | Tyr | Ser |
| | 85 | | | | 90 | | | | | 95 | | |
| 30 | Gly | Ala | Ala | Glu | Tyr | Leu | Tyr | Phe | Phe | Arg | Val | Leu |
| | | 100 | | | | | | 105 | | | | |
| | Val | Pro | Ala | Thr | Asp | Arg | Asn | Ala | Leu | Ser | Ser | Leu |
| | 110 | | | | 115 | | | | | | | 120 |
| | Trp | Gly | Lys | Leu | Ala | Ser | Glu | Ile | Leu | Met | Gln | Asn |
| | | | 125 | | | | | 130 | | | | |
| | Trp | Asp | Ala | Ala | Met | Glu | Asp | Leu | Thr | Arg | Leu | Lys |
| 35 | | 135 | | | | | | 140 | | | | |

| | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 0 | Glu | Thr | Ile | Asp | Asn | Ser | Val | Ser | Ser | Pro | Leu |
| | 145 | | | | 150 | | | | | 155 | |
| | Gln | Ser | Leu | Gln | Gln | Arg | Thr | Trp | Leu | Ile | His |
| | | | | 160 | | | | | 165 | | Trp |
| | Ser | Leu | Phe | Val | Phe | Phe | Asn | His | Pro | Lys | Gly |
| | 170 | | | | | | 175 | | | | 180 |
| | Asp | Asn | Ile | Ile | Asp | Leu | Phe | Leu | Tyr | Gln | Pro |
| | | | | | 185 | | | | | 190 | Gln |
| 5 | Tyr | Leu | Asn | Ala | Ile | Gln | Thr | Met | Cys | Pro | His |
| | | | 195 | | | | | 200 | | | Ile |
| | Leu | Arg | Tyr | Leu | Thr | Thr | Ala | Val | Ile | Thr | Asn |
| | 205 | | | | | | 210 | | | | 215 |
| | Asp | Val | Arg | Lys | Arg | Arg | Gln | Val | Leu | Lys | Asp |
| | | | | 220 | | | | | 225 | | Leu |
| | Val | Lys | Val | Ile | Gln | Gln | Glu | Ser | Tyr | Thr | Tyr |
| | 230 | | | | | | 235 | | | | 240 |
| 10 | Asp | Pro | Ile | Thr | Glu | Phe | Val | Glu | Cys | Leu | Tyr |
| | | | | | 245 | | | | | 250 | Val |
| | Asn | Phe | Asp | Phe | Asp | Gly | Ala | Gln | Lys | Lys | Leu |
| | | | 255 | | | | | 260 | | | Arg |
| | Glu | Cys | Glu | Ser | Val | Leu | Val | Asn | Asp | Phe | Phe |
| | 265 | | | | | 270 | | | | | 275 |
| | Val | Ala | Cys | Leu | Glu | Asp | Phe | Ile | Glu | Asn | Ala |
| | | | | 280 | | | | | 285 | | Arg |
| 15 | Leu | Phe | Ile | Phe | Glu | Thr | Phe | Cys | Arg | Ile | His |
| | 290 | | | | | | 295 | | | | Gln |
| | Cys | Ile | Ser | Ile | Asn | Met | Leu | Ala | Asp | Lys | Leu |
| | | | | | 305 | | | | | 310 | Asn |
| | Met | Thr | Pro | Glu | Glu | Ala | Glu | Arg | Trp | Ile | Val |
| | | | | | | | | 320 | | | Asn |
| 20 | Leu | Ile | Arg | Asn | Ala | Arg | Leu | Asp | Ala | Lys | Ile |
| | 325 | | | | | 330 | | | | | 335 |
| | Ser | Lys | Leu | Gly | His | Val | Val | Met | Gly | Asn | Asn |
| | | | | 340 | | | | | 345 | | Ala |
| | Val | Ser | Pro | Tyr | Gln | Gln | Val | Ile | Glu | Lys | Thr |
| | 350 | | | | | | 355 | | | | Lys |
| | Ser | Leu | Ser | Phe | Arg | Ser | Gln | Met | Leu | Ala | Met |
| | | | | | 365 | | | | | 370 | Asn |
| 25 | Ile | Glu | Lys | Lys | Leu | Asn | Gln | Asn | Ser | Arg | Ser |
| | | | | | | | | 380 | | | Glu |
| | Ala | Pro | Asn | Trp | Ala | Thr | Gln | Asp | Ser | Gly | Phe |
| | 385 | | | | | 390 | | | | | 395 |

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(xi) SEQUENCE DESCRIPTION:SEQ ID NO:5:

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° ACCAATAAAGTTTTAGTGAGCACAG 25

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base paris
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:6:

GCGCCCAAAGACCCCCTCAC 20

10

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:7:

TTAATCAGTTTCTTTGGGGA 20

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:8:

AGTTTCTAATGACAAACTTAC 22

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:9:

TCTTCTGCATTTTAAATTAG 20

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(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:10:

CAAAATTAAGACGAGTTTAC

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(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:11:

CTTATTTTGTTTCTGTGGCC

20

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:12:

CATGACAACTTTAAAATATTTTT

23

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:13:

AATTACAATGGGGTTTAAA

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° (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:14:

GAAGAACCAAGGGAATCCTA

20

(2) INFORMATION FOR SEQ ID NO:15:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:15:

15 TTCAAGAGTATTCACAATAT

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(2) INFORMATION FOR SEQ ID NO:16:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:16:

TGTGAAAAAGACGAACTCAC

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(2) INFORMATION FOR SEQ ID NO:17:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:17:

AGTTTTCTTTATCTCACCT

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35 (2) INFORMATION FOR SEQ ID NO:18:

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- ° (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:18:
5 CAATATATATTTTAGTTTAC 21
- (2) INFORMATION FOR SEQ ID NO:19:
- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:19:
15 CCGTTGACTTATTTTACAG 20
- (2) INFORMATION FOR SEQ ID NO:20:
- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:20:
AAATAAAAATTCACACTTAC 20
- 25 (2) INFORMATION FOR SEQ ID NO:21:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 30 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:21:
TTGTTGTATTTGTACATATAG 21
- (2) INFORMATION FOR SEQ ID NO:22:
- 35 (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:22:

5 ATCAAATCACGGTGTCTTAC 21

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION:SEQ ID NO:23:

AAACTAAGTTTTTAGGCC 20

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(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION:SEQ ID NO:24:

ATAGCTAACATAATACTCAC 20

(2) INFORMATION FOR SEQ ID NO:25:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:25:

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TTCCCTGTGTTTCCTTTTAG 20

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:30:

TGTATGTCATCCTTTATACA

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(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION:SEQ ID NO:31:

GTGAAAATGACATGAAATTTTCAG

23

(2) INFORMATION FOR SEQ ID NO:32:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:32:

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TGCAGTGTGACAATATGGGC

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